In the Specification:

Please amend the specification as shown:

Page 1, before paragraph [0001], please insert the following:

Sequence Listing

The instant application contains a "lengthy" Sequence Listing which has been submitted via CD-R in lieu of a printed paper copy, and is hereby incorporated by reference in its entirety. Said CD-R, recorded on April 26, 2006, are labeled CRF, "Copy 1" and "Copy 2", respectively, and each contains only one identical 888 Kb file (SEQ4072U.APP).

Please delete paragraph [0148] and replace it with the following paragraph:

[0148] When designing the siRNA molecules, the targeted region often is selected from a given DNA sequence beginning 50 to 100 nucleotides downstream of the start codon. See, e.g., Elbashir et al,. Methods 26:199-213 (2002). Initially, 5' or 3' UTRs and regions nearby the start codon were avoided assuming that UTR-binding proteins and/or translation initiation complexes may interfere with binding of the siRNP or RISC endonuclease complex. Sometimes regions of the target 23 nucleotides in length conforming to the sequence motif AA(N19)TT (SEQ ID NO: 18) (N, an nucleotide), and regions with approximately 30% to 70% G/C-content (often about 50% G/C-content) often are selected. If no suitable sequences are found, the search often is extended using the motif NA(N21). The sequence of the sense siRNA sometimes corresponds to (N19) TT or N21 (position 3 to 23 of the 23-nt motif), respectively. In the latter case, the 3' end of the sense siRNA often is converted to TT. The rationale for this sequence conversion is to generate a symmetric duplex with respect to the sequence composition of the sense and antisense 3' overhangs. The antisense siRNA is synthesized as the complement to position 1 to 21 of the 23-nt motif. Because position 1 of the 23-nt motif is not recognized sequencespecifically by the antisense siRNA, the 3'-most nucleotide residue of the antisense siRNA can be chosen deliberately. However, the penultimate nucleotide of the antisense siRNA

(complementary to position 2 of the 23-nt motif) often is complementary to the targeted sequence. For simplifying chemical synthesis, TT often is utilized. siRNAs corresponding to the target motif NAR(N17)YNN, where R is purine (A,G) and Y is pyrimidine (C,U), often are selected. Respective 21 nucleotide sense and antisense siRNAs often begin with a purine nucleotide and can also be expressed from pol III expression vectors without a change in targeting site. Expression of RNAs from pol III promoters often is efficient when the first transcribed nucleotide is a purine.

Please delete paragraph [0241] and replace it with the following paragraph:

[0241] For each polymorphism, SpectroDESIGNER™ software (Sequenom, Inc.) was used to generate a set of PCR primers and a MassEXTEND™ primer was used to genotype the polymorphism. Table 4 shows PCR primers and Table 5 shows extension primers used for analyzing polymorphisms. The initial PCR amplification reaction was performed in a 5 μl total volume containing 1X PCR buffer with 1.5 mM MgCl₂ (Qiagen), 200 μM each of dATP, dGTP, dCTP, dTTP (Gibco-BRL), 2.5 ng of genomic DNA, 0.1 units of HotStar DNA polymerase (Qiagen), and 200 nM each of forward and reverse PCR primers specific for the polymorphic region of interest.

TABLE 4: PCR Primers

Referenc e SNP ID	Forward PCR primer <u>(SEQ ID NOS 19-23)</u>	Reverse PCR primer (SEQ ID NOS 24-28)
rs1671152	ACGTTGGATGAGGGCCGCTT	ACGTTGGATGTGAACATCCTGTCGGCCTCC
rs1050348	CAGCTGGATGACTACAATGC	TGTTCATGTCTTCGGCATCC
rs454422	CAGCTTTTGAGGCACTTTCC	AGCACCTTGCATACCCATAG
rs763471	TAACTCCTGTGTGGCTTTCT	GTGAAGAGCTCTGAAATGCC
rs2046778	CATGAAGCCTTATGCTTGAG	GTTCCCTTCCCCCATAAAAC

Please delete paragraph [0243] and replace it with the following paragraph:

[0243] Once the SAP reaction was complete, a primer extension reaction was initiated by adding a polymorphism-specific MassEXTEND™ primer cocktail to each sample. Each MassEXTEND™ cocktail included a specific combination of dideoxynucleotides (dNTPs) and deoxynucleotides (dNTPs) used to distinguish polymorphic alleles from one another. In Table 5, ddNTPs are shown and the fourth nucleotide not shown is the dNTP.

TABLE 5: Extend Primers

Reference SNP ID	Extend Probe <u>(SEQ ID NOS 29-33)</u>	Term Mix
rs1671152	CTCCATCCTGACCCCCGT	ACT
rs1050348	CACTTGACCAGGCCCTTAAC	ACG
rs454422	GATCCTTCTCACTTACTGTTC	ACT
rs763471	CTCCAAGCAGTAAAGATGTTC	CGT
rs2046778	CTGTCATGATTGACAGGTCC	ACT

Please delete paragraph [0253] and replace it with the following paragraph:

[0253] The methods used to verify and allelotype the proximal SNPs of Table 7 are the same methods described in Examples 1 and 2 herein. The PCR primers and extend primers used in these assays are provided in Table 8 and Table 9, respectively.

TABLE 8

dbSNP rs#	Forward PCR primer (SEQ ID NOS 34-156)	Reverse PCR primer (SEQ ID NOS 157-279)
10666	ACGTTGGATGAGATGGCCCCTCTCCCCT	ACGTTGGATGAGTGGACTGGCCTGCAGGT
172006	ACGTTGGATGGGTTGAGGAGTATTCCATTG	ACGTTGGATGTGGGTGACAGCAAGACTCCA
269909	ACGTTGGATGAGTTTCTTGTCTCCTGGGTG	ACGTTGGATGCACAACAATGAAAGGACAAGC
269910	ACGTTGGATGGGCTGCTCAGGTTCTAAAAG	ACGTTGGATGCCCCAGTTCCTTATCTGATC
269911	ACGTTGGATGGGTGACAAAGTGAGACTCCG	ACGTTGGATGTGACTAGCTGGGATTATGGG
269912	ACGTTGGATGAGGAGAGCCTGCAGGTTGAA	ACGTTGGATGTCCCTTGATTGTCATCACAG
269913	ACGTTGGATGAGATGCACCGAATGGATCTG	ACGTTGGATGTCCTAGGACACAGTGTGGAC
269915	ACGTTGGATGAAGCTGAGATTGTGCTGCTG	ACGTTGGATGACTACTCTACTTTCTACCCC
269916	ACGTTGGATGAACTCCTGACCACGTGATCC	ACGTTGGATGAAAGTGTAGCTGGGCATGGC
703464	ACGTTGGATGAAAAGTAGCTGAGCGTGGTG	ACGTTGGATGCCCAGGTTCAAACAGTTCTC
703465	ACGTTGGATGGCTGTGATGACAATCAAGGG	ACGTTGGATGAGCAGGAACTGGCATTTGAG
703467	ACGTTGGATGAAACTTACGAAGGTCTGGGC	ACGTTGGATGGGGTTTCAGGAACATTCACC
703468	ACGTTGGATGGAAAGGAACAAGTGATCCAG	ACGTTGGATGCTTCTGAAAAAGGAGAAGGG
754235	ACGTTGGATGGTGGAACAACAGTTGGAGC	ACGTTGGATGGAGTGGAGATCATGCCATTG
775821	ACGTTGGATGTTTTCTCATCCGCCAGCAGG	ACGTTGGATGACAGAGCACAGGTCCCTTTC
775822	ACGTTGGATGAAAAGTAGAGCATGTGGACC	ACGTTGGATGGGGATGAACAGACAATCCTC
775894	ACGTTGGATGAGGCAGGAGGACTGATTGAG	ACGTTGGATGTTGTAGAGACAGGGTCTTGC
775900	ACGTTGGATGTCTGCAACGTTCGTTCTTCC	ACGTTGGATGTTCTTAATGTGCCCACTGTC
775903	ACGTTGGATGTGTGCCCGGCCCTTTTTTTC	ACGTTGGATGGGACTCCAGTCTGAGTGACA
776251	ACGTTGGATGAATCCTAGCTACTCAGGAGG	ACGTTGGATGATGGTATGATCTAGGCTCCC
892088	ACGTTGGATGATTGGTTACACTGGGACTGC	ACGTTGGATGAAGCGGTGATTCTCAGCCTC
892089	ACGTTGGATGCCCTACAAGAATCCCGAGAG	ACGTTGGATGAAGCTGTAGCATCGGTAGGTT
892090	ACGTTGGATGAAGCTGTAGCATCGGTAGGTT	ACGTTGGATGCCCTACAAGAATCCCGAGAG
892091	ACGTTGGATGAAGATGGAGGACCACAGGTG	ACGTTGGATGACCGGAATTACTGAGAGGTC
1036231	ACGTTGGATGAACAGTACTAAGGGCAGATG	ACGTTGGATGGTCCAGGGTGTTTACTGTTC

1036232	ACGTTGGATGCCAAAGAAACTCCCAGAATC	ACGTTGGATGGATCGTGCCATTGCACTTTG
1043673	ACGTTGGATGTGAAGTCATGAGAAGAAGGC	ACGTTGGATGGCTGCTGGAAGAAATAGAAG
1043678	ACGTTGGATGTTCATGATCTGAATCCCCCC	ACGTTGGATGGAACTCATTATCCCTGAGGG
1043680	ACGTTGGATGTCTAGCCCAGCAATGAACTC	ACGTTGGATGTTCCAGGTGTTGGTGAACTG
1043684	ACGTTGGATGCTCAATATACCCGTGATACAG	ACGTTGGATGTTTAGCCATGATTCTGCCTC
1054796	ACGTTGGATGAGTGTCACCCTGATTTCCAG	ACGTTGGATGCACCTTGGGAAATACGTTGC
1059211	ACGTTGGATGCTCAGCTCCTTGGTGAAGAG	ACGTTGGATGGGCAGACGAGGAAGTATAAC
1064675	ACGTTGGATGGAGTTCCCTCAGTTTTATTG	ACGTTGGATGCCTACTACATTCCTTTTTGC
1560714	ACGTTGGATGATCTGCTGACCTCGTGATCC	ACGTTGGATGAAAAGACAGTCTCAGGTGGG
1613662	ACGTTGGATGATGGACCCTGCAGAACCTAC	ACGTTGGATGTCTGATTTCCCAGGAACCTC
1625609	ACGTTGGATGTCAAGCGATTCTCCTGCCTC	ACGTTGGATGAAAAAATGAGCTGGGCGTGG
1625689	ACGTTGGATGGTAATCCCAGCTACTTGGAG	ACGTTGGATGATCTTGGCTCACTGCAGCCT
1626971	ACGTTGGATGTATTAAATGCACCTGGCACC	ACGTTGGATGCAAAGTGCTGGGATTACAGG
1654406	ACGTTGGATGCTTCTATTTCTTCCAGCAGC	ACGTTGGATGTTTCTTCCCCCATTGTACCC
1654409	ACGTTGGATGGTGAAACCTTGTCTCATATAC	ACGTTGGATGTGAGAGTAGGCATGTGGTAC
1654410	ACGTTGGATGACTGTGCCTAGGCTATACTG	ACGTTGGATGGGAAAATCATACTGAGATGC
1654411	ACGTTGGATGTGGAACTTCTTGGTGCCATC	ACGTTGGATGCCTGTAATCCCGGCACTTTG
1654412	ACGTTGGATGATTAGCCAGGTGTGGTGGTG	ACGTTGGATGTCAAGCCATTCTCCCACCTC
1654413	ACGTTGGATGAGGGCTGTGCAGAGGCCGCTT	ACGTTGGATGTCCATCCTGACCCCCGTTTG
1654415	ACGTTGGATGCCAAGAAAGTCCTTGGTGTG	ACGTTGGATGCTTTGAAATGGCCCCATCAC
1654416	ACGTTGGATGTCTGCTGAGCATGAAATGCC	ACGTTGGATGCTGAACTGACCGTCTCATTC
1654419	ACGTTGGATGTATCATACGCTAGGCTGGAG	ACGTTGGATGATGTTTCTCCTGCCTTGGTG
1654420	ACGTTGGATGCCAACCAACCAACAACCTG	ACGTTGGATGTGGAAGTTTGAGAACCGCTG
1654421	ACGTTGGATGAGGACACAGGAATCCAGAAG	ACGTTGGATGGCACATTCTGGGCTATTAAC
1654424	ACGTTGGATGTAGGTGGGAAGGAAGTGGGA	ACGTTGGATGCCACTTCTTTCCCACCTATG
1654425	ACGTTGGATGTACCTGTGACCACAAGCTCC	ACGTTGGATGTGCTACAGCTTCTCCAGCAG
1654438	ACGTTGGATGAATCAACTAGGCATGGTGGC	ACGTTGGATGCCAGGTTCAAGCGATTCTCC
1654439	ACGTTGGATGCCCCATATACATGTGCGATG	ACGTTGGATGAATGGGGTGTTTCTGGAGCA
1654441	ACGTTGGATGAGTAGCTGGGATTACAGGCG	ACGTTGGATGGGAGTTCAAGATAAGCCTGG
1654442	ACGTTGGATGAGGAGAATGGTGTGAAGCTG	ACGTTGGATGAATCTTGCTCTGTCACCCAG
1654444	ACGTTGGATGGGATGGTCCCAGTTTTACAT	ACGTTGGATGCCAGGAGAATCACTTTTATGG
1654446	ACGTTGGATGAAAAGGAAGGGCATTCTGGC	ACGTTGGATGTTTGGCCTCCCAAAGTACTG
1654447	ACGTTGGATGATCCCTGGGAAGACGGTCAT	ACGTTGGATGTTACCTCTCCTGGCCAGTTC
1654448	ACGTTGGATGTGCTCACTGCATGAGATTCC	ACGTTGGATGAACTTTGGCCTCCCAAAGTG
1654449	ACGTTGGATGAGTCCAGCCTGGCAAACATG	ACGTTGGATGCAGTCTAATCTCTCTTTTCCC
1654451	ACGTTGGATGTTTAAAATGCCCGCTGCACG	ACGTTGGATGAGGAGGATGCACTTATGTGG
1654452	ACGTTGGATGCTGTACGCATTACCACAGAC	ACGTTGGATGGTTTTGGACTCTTGACCTGC
1654459	ACGTTGGATGCAGGAGCTTGGGTACCCAC	ACGTTGGATGCCCTCATCTGGAAATGTGTG
1654485	ACGTTGGATGTTGTACCACTGCACTCTAGC	ACGTTGGATGCCTGACTCTACAGTTCTTGC
1654491	ACGTTGGATGCAGACGTCCGTGCTTCACC	ACGTTGGATGTCCAGGAACAGACGGAGGTC
1654495	ACGTTGGATGATGACCATTGCTCGTCTGTG	ACGTTGGATGGCTTTCTGCAGAGGTTGTCG
1654496	ACGTTGGATGAATCACAAATGGCAACACGG	ACGTTGGATGTTTGGATGCTGGCACTTGTG
1654497	ACGTTGGATGACCCCATGCTGTTTTCTC	ACGTTGGATGCAGAAGACTACCTGATTTGC
1654498	ACGTTGGATGCTTCCCACACCCACTATATC	ACGTTGGATGGTTAGTGAGTCGGTGACATC
1654499	ACGTTGGATGCACTACCTCTCTAGCAACTG	ACGTTGGATGACCTCAGATGATCTGCCCAC
1654503	ACGITGGATGTCCTTGGCTTGTGGCCCTTC	ACGTTGGATGAGCCAGGGCAACGTTTGAAG
1654504	ACGTTGGATGCCACCCCATGATTCCATTTC	ACGTTGGATGTGCTGTGATGCACCTTTGAC
1654505	ACGTTGGATGCCCTGTCTCTCTAAAACCAC	ACGTTGGATGATTCAAGCAGTTCTCGTGCC
1671133	ACGTTGGATGGTGGTCTCAACTTGGCTATC	ACGTTGGATGCCAGATAGGATTCCAGGTTC
10/1100	[10011001100101010101010110011100]	

1671140	ACGTTGGATGAGTCTGACAAGAGAGTCAGC	ACGTTGGATGTCCTTTACCTACCCACATCC
1671148	ACGTTGGATGGCCATCCTTCTGTCTTTTCC	ACGTTGGATGAGTGGCTCATGCCTGTAATC
1671149	ACGTTGGATGCTTTTCCCAAGTGACTCACC	ACGTTGGATGAAAAGAATGGCTGGCCACAG
1671150	ACGTTGGATGGTGCTATGATCAAATCAGGG	ACGTTGGATGACACCACTGCACTCTAGCTC
1671151	ACGTTGGATGGGAAAACCAGACAAGAGCAC	ACGTTGGATGTGACTCTGTTCCATCCTCTG
1671152	ACGTTGGATGAGGGCTGTGCAGAGGCCGCTT	ACGTTGGATGTGAACATCCTGTCGGCCTCC
1671153	ACGTTGGATGCCTACTCCGAACACACACAC	ACGTTGGATGATTATAGGCATGAGGCACCG
1671169	ACGTTGGATGTCCTGTTGCTGGACACTATC	ACGTTGGATGTCACACCTTCCGAGGATTAG
1671170	ACGTTGGATGAGGTGACAGTGCTGTACCTG	ACGTTGGATGACAAAGAACAGTGAGAGGGC
1671171	ACGTTGGATGAAGCAAGATACCGTCTCAGA	ACGTTGGATGCCGGGAAATGGAATAATTCC
1671176	ACGTTGGATGTGGAGCCACTTATGGAGAAC	ACGTTGGATGACCCCAACTGAAACACAGAC
1671178	ACGTTGGATGTAATCCCAGCACTTTGGGAG	ACGTTGGATGCATGTTTGCCAGGCTGGACT
1671182	ACGTTGGATGATAGGGCGGCTTTTCTCCTG	ACGTTGGATGCCTGGGAACTGAATGTCTCG
1671187	ACGTTGGATGAGTGCTCAGCAACGATTACG	ACGTTGGATGGAGGGCTGCAGGTTGAGAAA
1671188	ACGTTGGATGGAACCGCAGATGGACAATG	ACGTTGGATGAGATCACAGAGTGAGGAGAG
1671191	ACGTTGGATGTCGGACGCACACAGACTGTAG	ACGTTGGATGGGAAAGCGTATCTGCAGAGG
1671192	ACGTTGGATGTGGTAAGAGACGGACAGTTC	ACGTTGGATGTCAGCAGAAAGGAGTGTGAG
1671196	ACGTTGGATGTTGCTAGGCAACAGGCACTC	ACGTTGGATGTCTGTATCTGAGCCTCACTG
1671198	ACGTTGGATGATGAAACTAAGGCACATGGC	ACGTTGGATGCTTATAATCTACCCTCTTAGC
1671199	ACGTTGGATGGCTGAAATTTGCTAAGAGGG	ACGTTGGATGGACAGTTACTACTAGCAAGC
1671214	ACGTTGGATGAGGCGGAGAATGATCCGGTG	ACGTTGGATGACGCCATCATTCGTGCATCC
1671215	ACGTTGGATGTTCTCCAAAGCACCCAAGTG	ACGTTGGATGATGCTGGGCTTGCTTTTTCC
1671216	ACGTTGGATGTGCTTGGGAGCAAGTTACAG	ACGTTGGATGTTCCCCCTCCTGGTATTTAC
1671217	ACGTTGGATGTTGTCTCCATTCCTCCCTGG	ACGTTGGATGTCTTGTCTTGCCCTCTCGCT
1671218	ACGTTGGATGTGAGTCTGGTAGGCAACTTC	ACGTTGGATGTAGAAGCCAGTCGCTACATC
1671219	ACGTTGGATGTGATCTCGGCTCACTGCAAG	ACGTTGGATGAAATTAGCTGGGCATGGTGG
1671221	ACGTTGGATGTGGTGAAACCCCATTTCTAC	ACGTTGGATGGGTTCAAGGGATTCTCCTGC
1671223	ACGTTGGATGTCAAGTGATTCTCCTGCCTC	ACGTTGGATGCCCACCTCTACTGAAAATAC
1671224	ACGTTGGATGTGAGTCTCACTCTTGTTGCC	ACGTTGGATGCAGGAGAATCACTTGAACCC
1671225	ACGTTGGATGTATAGGCGTGAGCCACTATG	ACGTTGGATGCTATTGGAAGCTACATGCTC
1671226	ACGTTGGATGTATTGGCCAGACTGGACTTC	ACGTTGGATGAGTTACTCAGGAGGCTAAGG
1671227	ACGTTGGATGGGTTTCTGTTCAGAGATTCG	ACGTTGGATGTGCAGTGAGCCTAGATCATG
1671228	ACGTTGGATGTCAGCCTCCCAGGGATTAAG	ACGTTGGATGACATGGTGAAAACTCGTCTC
1869616	ACGTTGGATGTAATCCCAGCTACTCGGAAG	ACGTTGGATGACGGTGGCTCACTTCAACCT
2019599	ACGTTGGATGGTGCTGGGATTATAGGCATG	ACGTTGGATGTACTCCGAACACACACACAC
2116883	ACGTTGGATGATTACAGGCATGAGCCACTG	ACGTTGGATGCACGCGCAGTTCAATTTCTC
2124090	ACGTTGGATGTCTGACAAAGCTGGAAGCTG	ACGTTGGATGCTGATAAACAAGGCTGTGGG
2163833	ACGTTGGATGGATATTGGTGAGTATGCAGAG	ACGTTGGATGAACTGTTTTCCACAGCAGGG
2217659	ACGTTGGATGTTCCCCCCTTCTCCTTTTTC	ACGTTGGATGATGAGGTAACTTACCTAATG
2304167	ACGTTGGATGGTTTGGTTCCCAGAGACTTC	ACGTTGGATGAGGATGACTTACTCACCAGC
2304168	ACGTTGGATGTCAGCAGAAAGGAGTGTGAG	ACGTTGGATGTGGTAAGAGACGGACAGTTC
2365593	ACGTTGGATGTGACGCAGTAAGACTCCATC	ACGTTGGATGCAAAGTGCTGGGATTACAGG
2365721	ACGTTGGATGTTGTACAGCCTGCAAGCAAC	ACGTTGGATGAGATCGCGCCATTGCACTCA
2569513	ACGTTGGATGGTTGGCGTTTTTGTTTGCAC	ACGTTGGATGTCTCATAGTATTCTGCAGGG
2569514	ACGTTGGATGTCCCTGCAGAATACTATGAG	ACGTTGGATGAGAGTGTTGGGATTACAGGC
2886414	ACGTTGGATGGGTGTGCTTTACAAATGCTG	ACGTTGGATGAACTGAGATCACTCCACTGC
2886415	ACGTTGGATGTGACGCAGTAAGACTCCATC	ACGTTGGATGCAAAGTGCTGGGATTACAGG
3745912	ACGTTGGATGACGTCTTCTGAGGCACAGAG	ACGTTGGATGGCTGTTAGAGGCTGGCAGG
3786863	ACGTTGGATGTGACCAACAGAAGTCTCAGG	ACGTTGGATGTTGACCTCAGGTGATCCATC

TABLE 9

dbSNP rs#	Extend Primer (SEQ ID NOS 280-402)	Term Mix
10666	TGCAGGTGAGCACTGCCC	ACG
172006	GCAAGACTCCATCTCAA	ACT
269909	AAGCATAGATCAGATAAGGAA	ACT
269910	ATCTATGCTTGTCCTTTCAT	ACT
269911	GCTCAGCTACTTTTTGTAT	CGT
269912	CAAGATGGTGTCTTCGGC	ACT
269913	ACAGTGTGGACCGATTTCC	ACT
269915	AGACAAGTCTCACTCTG	ACG
269916	GGCGGCTCACACCTGTAAT	ACG
703464	CTCCTGCCTCAGCCTCC	ACG
703465	TGGCATTTGAGACAGGA	ACT
703467	CATTCACCATGTCTGTGAG	ACG
703468	CTTCATAAAAGAAAAGATGACA	ACG
754235	CATGCCATTGTACTCCAGCC	ACG
775821	CCTGCCAGCCTCTAACAGC	ACG
775822	TAGTGATGTCTGCTTCAG	ACT
775894	TTGCCCAGGCTGGCCTC	ACT
775900	GAATGCCAACCTCCCTTCC	ACT
775903	TCTGAGTGACAGAGCGA	ACT
776251	GCTCCCGCAACCTCCGC	ACG
892088	GCCTCGGCCGCAATCACA	ACT
892089	CGGTCACCGTGATGATGGG	ACT
892090	AGAATCCCGAGAGATGGTAC	CGT
892091	GTCCTTCACCTGAGCTTCC	ACT
1036231	GTGTTTACTGTTCAAGGCAAGT	ACT
1036232	GGCAACAGAGCAAGACT	ACG
1043673	ACTGAGAAACATCATCCCTGGG	CGT
1043678	AGTCACAGGCAGTTCACC	CGT
1043680	CTGTGACTCCTCTCCCC	ACT
1043684	CTGTTTTATACCTGCACAC	ACT
1054796	ACGCCAGGCAGGCTCTCA	ACT
1059211	CGCCTACTGCCAGAGCAAGCT	ACG
1064675	ATTCCTTTTTGCTGAAATAATGAA	ACT
1560714	TGGGGCGTGATGGCTCA	ACG
1613662	CAACAGAACCACCTTCC	ACG
1625609	GTGCACACCTGTAATCC	ACG
1625689	CAGGGCTCAAGCGATTCTCC	ACG
1626971	TCGCCTGGCCAAAAAA	ACT
1654406	CATTGTACCCCAGGTTGAAAAT	CGT
1654409	GTGGTACCACACCCAGCTAATT	ACT
1654410	ATCATACTGAGATGCTATCAGAA	ACT
1654411	GCACTTTGGGAGGTTGAGG	ACT

1654412	CATTCTCCCACCTCAGCCCCC	ACG
1654413	CCCGTTTGATTTCCGGGTC	CGT
1654415	GGCCCCATCACCCAAAA	ACG
1654416	GACCGTCTCATTCACAAAC	ACT
1654419	TTGGTGCTTCACTCTGAGAC	ACT
1654420	GAGAACCGCTGATCAATGCA	CGT
1654421	GCATGCAGCTCCCGTCC	ACT
1654424	CCACCTATGGCCGCGCCCCT	ACT
1654425	CAGGGACCCATACCTGTGGTC	ACT
1654438	TCAGCCTCCTGAGTAGCTGG	ACT
1654439	GTTTCTGGAGCACTCCGGT	ACT
1654441	GATAAGCCTGGCCAACA	ACG
1654442	ATGATCTCGGCTCACTGCAA	ACT
1654444	TATGGATCTTTCTAGTCTTGTTT	CGT
1654446	ACTGATTACAGGCGTGC	ACT
1654447	CCCGATGCCTGTGTTGGC	ACT
1654448	AGTGCTGGGATTACAGG	ACG
1654449	AATCTCTCTTTTCCCTACACA	ACG
1654451	TAATGCGTACAGCAGCC	CGT
1654452	ACTGGAGGAGGATGCACTTA	ACG
1654459	ATGCACAGAAACAAGGATCTA	ACT
1654485	, CTTGCTTTTTTTTTTTGGACAG	ACT
1654491	GCACCCGAGCCTTTCCAG	ACT
1654495	TTGTCGTAAGTCTCTCCTCTTT	CGT
1654496	CGGGAAGGTTGAAGTTGGAC	CGT
1654497	CCATTTACAACCAATTGC	ACT
1654498	CTTGTGGGACTTCTTTTTA	ACT
1654499	ACCCTGGCCTCCCTAAC	ACT
1654503	GGGCAACGTTTGAAGATGCTCTGC	ACG
1654504	CACCTTTGACTCTTGAGCC	ACT
1654505	TAGCTATGTGCCACCATGCC	ACG
1671133	GATTGTAGCTAACTCACAAGG	ACT
1671140	TACCTACCCACATCCTATAAAA	ACG
1671148	CCTGTAATCCCGGCACT	ACT
1671149	CTGGCCACAGTGGCTCA	ACG
1671150	CGGGTGACGAAGCCTGAC	ACG
1671151	TCCTCTGTGCAAAATCCTCC	ACG
1671152	CTCCATCCTGACCCCCGT	ACT
1671153	CTGTGGAATTGTGCCTC	CGT
1671169	CATGTCCCACAGAGGCTAAC	ACT
1671170	GAGAGGCAATGCCTCAGAG	CGT
1671171	TTCTGGGATTCTCTAGAGGG	ACT
1671176	AGACATCATCACATCACACCA	CGT
1671178	CCAGGCTGGACTCGAACT	ACG
1671182	ACTGAATGTCTCGGTATAAAACC	ACG
1671187	CAGGTTGAGAAAGCTCTA	CGT

1671188 CAGAGTGAGGAGAGTGAGAC ACT 1671191 GAGCGGTTAGAAGATGTGCT ACT 1671192 AAGCCTGTAGGCTTTTAA ACG 1671196 GGGATGACTGAATGAGACAGTA ACG 1671198 CCCTCTTAGCAAATTTCAGCT ACT 1671199 TAACTTTTTTGTGTGAGAA ACG 1671214 CGTGCATCCTTCCCACCTA ACG 1671215 GTACTCAAGATGATGTAA CGT 1671216 TTACACCCTGGAGTGGTCC ACT 1671217 TGCCCTCTCGCTGGCTGG ACG 1671218 CAAAGGGAGTGGTCGCAC ACG 1671219 CAGGAGAATGGTGAACC ACG 1671221 AGCTGGGATTACAGGCA ACG 1671222 AGCTGGGATTACAGGCA ACG 1671223 TACAAAATTAGCTGGGCATG ACT 1671224 CTGTGAGCCGAGATTGC ACT 1671225 CTCAATGTGATTGCCACT ACT 1671226 GCAGGAGATCACTTGAACTT ACT 1671227 AGATCATGCCATTGCCAGC ACT 1671228 ACAGAAGTAGACCACTGGG ACT			,
1671192 AAGCCTGTAGGCTTTTAA ACG 1671196 GGGATGACTGAATGAGACAGTA ACG 1671198 CCCTCTTAGCAAATTTCAGCT ACT 1671199 TAACTTTTTTGTGTGTGAGAA ACG 1671214 CGTGCATCCTTCCCACCTA ACG 1671215 GTACTCAAGATGATAA CGT 1671216 TTACACCCTGGAGTGGTCC ACT 1671217 TGCCCTCTCGCTGGCTGG ACG 1671218 CAAAGGAGTGGTCGCAC ACG 1671219 CAGGAGAATGGTGTGAACC ACG 1671221 AGCTGGGATTACAGGCA ACG 1671223 TACAAAATTAGCTGGGCATG ACT 1671224 CTGTGAGCCGAGATTGC ACT 1671225 CTCAATGTGATCCTCCT ACT 1671226 GCAGGAGAATCACTTGAACTT ACT 1671227 AGATCATGCCATTGCCAGC ACT 1671228 ACAGAAGTTAGCTGGGC ACT 1869616 CTTCAACCTCCGCCTCCTGG ACT 2019599 GAAAAGCATGGGCCGGGCA ACG 2116883 CATACTCACCAATATCTGCT ACT <tr< td=""><td>1671188</td><td>CAGAGTGAGGAGAGTGAGAC</td><td>ACT</td></tr<>	1671188	CAGAGTGAGGAGAGTGAGAC	ACT
1671196 GGGATGACTGAATGAGACAGTA ACG 1671198 CCCTCTTAGCAAATITCAGCT ACT 1671199 TAACTTTTTTGTGTGTGAGAA ACG 1671214 CGTGCATCCTTCCCACCTA ACG 1671215 GTACTCAAGATGATAA CGT 1671216 TTACACCCTGGAGTGGTCC ACT 1671217 TGCCCTCTCGCTGGCTGG ACG 1671218 CAAAGGGAGGTGGTCGCAC ACG 1671219 CAGGAGAATGGTGGAACC ACG 1671221 AGCTGGGATTACAGGCA ACG 1671223 TACAAAATTAGCTGGGCATG ACT 1671224 CTGTGAGCCGAGATTGC ACT 1671225 CTCAATGTGATCCTCCT ACT 1671226 GCAGGAGAATCACTTGAACTT ACT 1671227 AGATCATGCCATTGCCAGC ACT 1671228 ACAGAAGTTAGCTGGGC ACT 1869616 CTTCAACCTCCGCCTCCTGG ACT 2019599 GAAAAGCATGGGCCAGGCA ACG 2116883 CATACTCACCAATATCTGCT ACT 2163833 GCCAGCAATGCACCACGC ACG <t< td=""><td>1671191</td><td>GAGCGGTTAGAAGATGTGCT</td><td>ACT</td></t<>	1671191	GAGCGGTTAGAAGATGTGCT	ACT
1671198 CCCTCTTAGCAAATTTCAGCT ACT 1671199 TAACTTTTTTGTGTGTGAGAA ACG 1671214 CGTGCATCCTTCCCACCTA ACG 1671215 GTACTCAAGATGATGAA CGT 1671216 TTACACCCTGGATGGTCC ACT 1671217 TGCCCTCTCGCTGGCTGG ACG 1671218 CAAAGGGAGTGGTCGCAC ACG 1671219 CAGGAGAATGGTGTGAACC ACG 1671221 AGCTGGGATTACAGGCA ACG 1671223 TACAAAATTAGCTGGGCATG ACT 1671224 CTGTGAGCCGAGATTGC ACT 1671225 CTCAATGTGATCCTCCT ACT 1671226 GCAGGAGAATCACTTGAACTT ACT 1671227 AGATCATGCCATTGCCAGC ACT 1671228 ACAGAAGTTAGCTGGGC ACT 1869616 CTTCAACCTCCGCCTCCTGG ACT 2019599 GAAAAGCATGGGCCGGCA ACG 2116883 CATACTCACCAATATCTGCT ACT 2163833 GCCAGCAATGCACGCGCAGT ACG 2217659 GTAACTTACCTAATGATAGAGG ACG <	1671192	AAGCCTGTAGGCTTTTAA	ACG
1671199 TAACTTTTTTGTGTGTGAGAA ACG 1671214 CGTGCATCCTTCCCACCTA ACG 1671215 GTACTCAAGATGATGTAA CGT 1671216 TTACACCCTGGAGTGGTCC ACT 1671217 TGCCCTCTCGCTGGCTGG ACG 1671218 CAAAGGGAGGTGGTCGCAC ACG 1671219 CAGGAGAATGGTGGAACC ACG 1671221 AGCTGGGATTACAGGCA ACG 1671223 TACAAAATTAGCTGGGCATG ACT 1671224 CTGTGAGCCGAGATTGC ACT 1671225 CTCAATGTGATCCTCCT ACT 1671226 GCAGGAGAATCACTTGAACTT ACT 1671227 AGATCATGCCATTGCCAGC ACT 1671228 ACAGAAGTTAGCTGGGC ACT 1869616 CTTCAACCTCCGCCTCCTGG ACT 2019599 GAAAAGCATGGGCCGGGCA ACG 2116883 CATACTCACCAATATCTGCT ACT 2163833 GCCAGCAATGCACGCGCAGT ACG 2217659 GTAACTTACCTAATGATAGAGG ACG 2304168 CAGTTCGGTGAAGTGGT ACT <t< td=""><td>1671196</td><td>GGGATGACTGAATGAGACAGTA</td><td>ACG</td></t<>	1671196	GGGATGACTGAATGAGACAGTA	ACG
1671214 CGTGCATCCTTCCCACCTA ACG 1671215 GTACTCAAGATGATGTAA CGT 1671216 TTACACCCTGGATGGTCC ACT 1671217 TGCCCTCTCGCTGGCTGG ACG 1671218 CAAAGGGAGTGGTCGCAC ACG 1671219 CAGGAGAATGGTGTGAACC ACG 1671221 AGCTGGGATTACAGGCA ACG 1671223 TACAAAATTAGCTGGGCATG ACT 1671224 CTGTGAGCCGAGATTGC ACT 1671225 CTCAATGTGATCCTCT ACT 1671226 GCAGGAGAATCACTTGAACTT ACT 1671227 AGATCATGCCATTGCCAGC ACT 1671228 ACAGAAGTTAGCTGGGC ACT 1869616 CTTCAACCTCCGCCTCCTGG ACT 2019599 GAAAAGCATGGGCCGGGCA ACG 2116883 CATACTCACCAATATCTGCT ACT 2163833 GCCAGCAATGCACGCGCAGT ACG 2217659 GTAACTTACCTAATGATAGAGG ACG 2304167 TGACTCCTTTGGACTGG ACG 2304168 CAGTTCGGTGAAGTGGT ACG	1671198	CCCTCTTAGCAAATTTCAGCT	ACT
1671215 GTACTCAAGATGATGTAA CGT 1671216 TTACACCCTGGAGTGGTCC ACT 1671217 TGCCCTCTCGCTGGCTGG ACG 1671218 CAAAGGGAGGTGGTCGCAC ACG 1671219 CAGGAGAATGGTGTAACC ACG 1671221 AGCTGGGATTACAGGCA ACG 1671223 TACAAAATTAGCTGGGCATG ACT 1671224 CTGTGAGCCGAGATTGC ACT 1671225 CTCAATGTGATCCTCCT ACT 1671226 GCAGGAGAATCACTTGAACTT ACT 1671227 AGATCATGCCATTGCCAGC ACT 1671228 ACAGAAGTTAGCTGGGC ACT 1869616 CTTCAACCTCCGCCTCCTGG ACT 2019599 GAAAAGCATGGGCCGGCAA ACG 2116883 CATACTCACCAATATCTGCT ACT 2124090 GCTTTGTGTTCTTTCTAGTC ACT 2163833 GCCAGCAATGCACGCGCAGT ACG 2217659 GTAACTTACCTAATGATAGAGG ACG 2304167 TGACTCCTTTGGACTGG ACG 2304168 CAGTTCGGTGAAGTGGT ACG	1671199	TAACTTTTTTGTGTGTGAGAA	ACG
1671216 TTACACCCTGGAGTGGTCC ACT 1671217 TGCCCTCTCGCTGGCTGG ACG 1671218 CAAAGGGAGGTGGTCGCAC ACG 1671219 CAGGAGAATGGTGTAACC ACG 1671221 AGCTGGGATTACAGGCA ACG 1671223 TACAAAATTAGCTGGGCATG ACT 1671224 CTGTGAGCCGAGATTGC ACT 1671225 CTCAATGTGATCCTCCT ACT 1671226 GCAGGAGAATCACTTGAACTT ACT 1671227 AGATCATGCCATTGCCAGC ACT 1671228 ACAGAAGTTAGCTGGGC ACT 1869616 CTTCAACCTCCGCCTCCTGG ACT 2019599 GAAAAGCATGGGCCGGGCA ACG 2116883 CATACTCACCAATATCTGCT ACT 2163833 GCCAGCAATGCACGCGCAGT ACG 2217659 GTAACTTACCTAATGATAGAGG ACG 2304167 TGACTCCTTTGGACTGG ACG 2304168 CAGTTCGGTGAAGTGGTT ACT 2365593 GGTGGGAGCCACCACGCC ACG 2365721 AGACTCCCTCTCAAAATAA ACG	1671214	CGTGCATCCTTCCCACCTA	ACG
1671217 TGCCCTCTCGCTGGCTGG ACG 1671218 CAAAGGGAGGTGGTCGCAC ACG 1671219 CAGGAGAATGGTGTGAACC ACG 1671221 AGCTGGGATTACAGGCA ACG 1671223 TACAAAATTAGCTGGGCATG ACT 1671224 CTGTGAGCCGAGATTGC ACT 1671225 CTCAATGTGATCCTCCT ACT 1671226 GCAGGAGAATCACTTGAACTT ACT 1671227 AGATCATGCCATTGCCAGC ACT 1671228 ACAGAAGTTAGCTGGGC ACT 1869616 CTTCAACCTCCGCCTCCTGG ACT 2019599 GAAAAGCATGGGCCGGGCA ACG 2116883 CATACTCACCAATATCTGCT ACT 2124090 GCTTTGTGTTCTTTCTAGTC ACT 2163833 GCCAGCAATGCACGCGCAGT ACG 2217659 GTAACTTACCTAATGATAGAGG ACG 2304167 TGACTCCTTTGGACTGG ACG 2304168 CAGTTCGGTGAAGTGGTT ACT 2365593 GGTGGCACCACCACGCC ACG 2365721 AGACTCCCCTCTCAAAATAA ACG <tr< td=""><td>1671215</td><td>GTACTCAAGATGATGTAA</td><td>CGT</td></tr<>	1671215	GTACTCAAGATGATGTAA	CGT
1671218 CAAAGGGAGGTGGTCGCAC ACG 1671219 CAGGAGAATGGTGTGAACC ACG 1671221 AGCTGGGATTACAGGCA ACG 1671223 TACAAAATTAGCTGGGCATG ACT 1671224 CTGTGAGCCGAGATTGC ACT 1671225 CTCAATGTGATCCTCCT ACT 1671226 GCAGGAGAATCACTTGAACTT ACT 1671227 AGATCATGCCATTGCCAGC ACT 1671228 ACAGAAGTTAGCTGGGC ACT 1869616 CTTCAACCTCCGCCTCCTGG ACT 2019599 GAAAAGCATGGGCCGGGCA ACG 2116883 CATACTCACCAATATCTGCT ACT 2124090 GCTTTTGTTTTTTAGTC ACT 2163833 GCCAGCAATGCACGCGCAGT ACG 2217659 GTAACTTACCTAATGATAGAG ACG 2304167 TGACTCCTTTGGACTGG ACG 2304168 CAGTTCGGTGAAGTGGTT ACT 2365593 GGTGTGAGCCACCACGCC ACG 2365721 AGACTCCCTCTCAAAATAA ACG 2569513 AGGGATAAGCATGAAACCACT ACG	1671216	TTACACCCTGGAGTGGTCC	ACT
1671219 CAGGAGAATGGTGTGAACC ACG 1671221 AGCTGGGATTACAGGCA ACG 1671223 TACAAAATTAGCTGGGCATG ACT 1671224 CTGTGAGCCGAGATTGC ACT 1671225 CTCAATGTGATCCTCCT ACT 1671226 GCAGGAGAATCACTTGAACTT ACT 1671227 AGATCATGCCATTGCCAGC ACT 1671228 ACAGAAGTTAGCTGGGC ACT 1869616 CTTCAACCTCCGCCTCCTGG ACT 2019599 GAAAAGCATGGGCCGGGCA ACG 2116883 CATACTCACCAATATCTGCT ACT 2124090 GCTTTGTGTTCTTTCTAGTC ACT 2163833 GCCAGCAATGCACGCGCAGT ACG 2217659 GTAACTTACCTAATGATAGAGG ACG 2304167 TGACTCCTTTGGACTGG ACG 2304168 CAGTTCGGTGAAGTGGTT ACT 2365593 GGTGTGAGCCACCACGCC ACG 2365721 AGACTCCCTCTCAAAATAA ACG 2569513 AGGGATAAGCATGAACCACT ACG 2569514 GCGTGACACACGCC ACG	1671217	TGCCCTCTCGCTGGCTGG	ACG
1671221 AGCTGGGATTACAGGCA ACG 1671223 TACAAAATTAGCTGGGCATG ACT 1671224 CTGTGAGCCGAGATTGC ACT 1671225 CTCAATGTGATCCTCCT ACT 1671226 GCAGGAGAATCACTTGAACTT ACT 1671227 AGATCATGCCATTGCCAGC ACT 1671228 ACAGAAGTTAGCTGGGC ACT 1869616 CTTCAACCTCCGCCTCCTGG ACT 2019599 GAAAAGCATGGGCCGGGCA ACG 2116883 CATACTCACCAATATCTGCT ACT 2124090 GCTTTGTGTTCTTTCTAGTC ACT 2163833 GCCAGCAATGCACGCGCAGT ACG 2217659 GTAACTTACCTAATGATAGAGG ACG 2304167 TGACTCCTTTGGACTGG ACG 2304168 CAGTTCGGTGAAGTGGTT ACT 2365593 GGTGTGAGCCACCACGCC ACG 2365721 AGACTCCCTCTCAAAATAA ACG 2569513 AGGGATAAGCATGAAACCACT ACG 2869514 GCGTGAGCCACCACGCC ACG 2886415 CACGCCTGGCTAAGCCT ACT	1671218	CAAAGGGAGGTGGTCGCAC	ACG
1671223 TACAAAATTAGCTGGGCATG ACT 1671224 CTGTGAGCCGAGATTGC ACT 1671225 CTCAATGTGATCCTCCT ACT 1671226 GCAGGAGAATCACTTGAACTT ACT 1671227 AGATCATGCCATTGCCAGC ACT 1671228 ACAGAAGTTAGCTGGGC ACT 1869616 CTTCAACCTCCGCCTCCTGG ACT 2019599 GAAAAGCATGGGCCGGGCA ACG 2116883 CATACTCACCAATATCTGCT ACT 2124090 GCTTTGTGTTCTTTCTAGTC ACT 2163833 GCCAGCAATGCACGCGCAGT ACG 2217659 GTAACTTACCTAATGATAGAGG ACG 2304167 TGACTCCTTTGGACTGG ACG 2304168 CAGTTCGGTGAAGTGGTT ACT 2365593 GGTGTGAGCCACCACGCC ACG 2365721 AGACTCCCTCTCAAAATAA ACG 2569513 AGGGATAAGCATGAAACCACT ACG 2569514 GCGTGAGCCACCACGCC ACG 2886414 GGGTGACAAAGTGAGACTC ACG 2886415 CACGCCTGGCTAAGCCT ACT <t< td=""><td>1671219</td><td>CAGGAGAATGGTGTGAACC</td><td>ACG</td></t<>	1671219	CAGGAGAATGGTGTGAACC	ACG
1671224 CTGTGAGCCGAGATTGC ACT 1671225 CTCAATGTGATCCTCCT ACT 1671226 GCAGGAGAATCACTTGAACTT ACT 1671227 AGATCATGCCATTGCCAGC ACT 1671228 ACAGAAGTTAGCTGGGC ACT 1869616 CTTCAACCTCCGCCTCCTGG ACT 2019599 GAAAAGCATGGGCCGGGCA ACG 2116883 CATACTCACCAATATCTGCT ACT 2124090 GCTTTGTGTTCTTTCTAGTC ACT 2163833 GCCAGCAATGCACGCGCAGT ACG 2217659 GTAACTTACCTAATGATAGAGG ACG 2304167 TGACTCCTTTGGACTGG ACG 2304168 CAGTTCGGTGAAGTGGTT ACT 2365593 GGTGTGAGCCACCACGCC ACG 2365721 AGACTCCCTCTCAAAATAA ACG 2569513 AGGGATAAGCATGAAACCACT ACG 2569514 GCGTGAGCCACCACGCC ACG 2886414 GGGTGACAAAGTGAGCCT ACG 2886415 CACGCCTGGCTAAGCCT ACT 3745912 GGCTGGCAGGCCAGGTCAAC ACT <td>1671221</td> <td>AGCTGGGATTACAGGCA</td> <td>ACG</td>	1671221	AGCTGGGATTACAGGCA	ACG
1671225 CTCAATGTGATCCTCT ACT 1671226 GCAGGAGAATCACTTGAACTT ACT 1671227 AGATCATGCCATTGCCAGC ACT 1671228 ACAGAAGTTAGCTGGGC ACT 1869616 CTTCAACCTCCGCCTCCTGG ACT 2019599 GAAAAGCATGGGCCGGGCA ACG 2116883 CATACTCACCAATATCTGCT ACT 2124090 GCTTTGTGTTCTTTCTAGTC ACT 2163833 GCCAGCAATGCACGCGCAGT ACG 2217659 GTAACTTACCTAATGATAGAGG ACG 2304167 TGACTCCTTTGGACTGG ACG 2304168 CAGTTCGGTGAAGTGGTT ACT 2365593 GGTGTGAGCCACCACGCC ACG 2365721 AGACTCCCTCTCAAAATAA ACG 2569513 AGGGATAAGCATGAAACCACT ACG 2569514 GCGTGAGCCACCACGCC ACG 2886414 GGGTGACAAAGTGAGACTC ACG 2886415 CACGCCTGGCTAAGCCT ACT 3745912 GGCTGGCAGGCCAGGTCAAC ACT	1671223	TACAAAATTAGCTGGGCATG	ACT
1671226 GCAGGAGAATCACTTGAACTT ACT 1671227 AGATCATGCCATTGCCAGC ACT 1671228 ACAGAAGTTAGCTGGGC ACT 1869616 CTTCAACCTCCGCCTCCTGG ACT 2019599 GAAAAGCATGGGCCGGGCA ACG 2116883 CATACTCACCAATATCTGCT ACT 2124090 GCTTTGTGTTCTTTCTAGTC ACT 2163833 GCCAGCAATGCACGCGCAGT ACG 2217659 GTAACTTACCTAATGATAGAGG ACG 2304167 TGACTCCTTTGGACTGG ACG 2304168 CAGTTCGGTGAAGTGGTT ACT 2365593 GGTGTGAGCCACCACGCC ACG 2365721 AGACTCCCTCTCAAAATAA ACG 2569513 AGGGATAAGCATGAAACCACT ACG 2569514 GCGTGAGCCACCACGCC ACG 286414 GGGTGACAAAGTGAGACTC ACG 2886415 CACGCCTGGCTAAGCCT ACT 3745912 GGCTGGCAGGCCAGGTCAAC ACT	1671224	CTGTGAGCCGAGATTGC	ACT
1671227 AGATCATGCCATTGCCAGC ACT 1671228 ACAGAAGTTAGCTGGGC ACT 1869616 CTTCAACCTCCGCCTCCTGG ACT 2019599 GAAAAGCATGGGCCGGGCA ACG 2116883 CATACTCACCAATATCTGCT ACT 2124090 GCTTTGTGTTCTTTCTAGTC ACT 2163833 GCCAGCAATGCACGCGCAGT ACG 2217659 GTAACTTACCTAATGATAGAGG ACG 2304167 TGACTCCTTTGGACTGG ACG 2304168 CAGTTCGGTGAAGTGGTT ACT 2365593 GGTGTGAGCCACCACGCC ACG 2365721 AGACTCCCTCTCAAAATAA ACG 2569513 AGGGATAAGCATGAAACCACT ACG 2569514 GCGTGAGCCACCACGCC ACG 286414 GGGTGACAAAGTGAGACTC ACG 2886415 CACGCCTGGCTAAGCCT ACT 3745912 GGCTGGCAGGCCAGGTCAAC ACT	1671225	CTCAATGTGATCCTCCT	ACT
1671228 ACAGAAGTTAGCTGGGC ACT 1869616 CTTCAACCTCCGCCTCCTGG ACT 2019599 GAAAAGCATGGGCCGGGCA ACG 2116883 CATACTCACCAATATCTGCT ACT 2124090 GCTTTGTGTTCTTTCTAGTC ACT 2163833 GCCAGCAATGCACGCGCAGT ACG 2217659 GTAACTTACCTAATGATAGAGG ACG 2304167 TGACTCCTTTGGACTGG ACG 2304168 CAGTTCGGTGAAGTGGTT ACT 2365593 GGTGTGAGCCACCACGCC ACG 2365721 AGACTCCCTCTCAAAATAA ACG 2569513 AGGGATAAGCATGAAACCACT ACG 2569514 GCGTGAGCCACCACGCC ACG 286414 GGGTGACAAAGTGAGACTC ACG 2886415 CACGCCTGGCTAAGCCT ACT 3745912 GGCTGGCAGGCCAGGTCAAC ACT	1671226	GCAGGAGAATCACTTGAACTT	ACT
1869616 CTTCAACCTCCGCCTCCTGG ACT 2019599 GAAAAGCATGGGCCGGGCA ACG 2116883 CATACTCACCAATATCTGCT ACT 2124090 GCTTTGTGTTCTTTCTAGTC ACT 2163833 GCCAGCAATGCACGCGCAGT ACG 2217659 GTAACTTACCTAATGATAGAGG ACG 2304167 TGACTCCTTTGGACTGG ACG 2304168 CAGTTCGGTGAAGTGGTT ACT 2365593 GGTGTGAGCCACCACGCC ACG 2365721 AGACTCCCTCTCAAAATAA ACG 2569513 AGGGATAAGCATGAAACCACT ACG 2569514 GCGTGAGCCACCACGCC ACG 286414 GGGTGACAAAGTGAGACTC ACG 2886415 CACGCCTGGCTAAGCCT ACT 3745912 GGCTGGCAGGCCAGGTCAAC ACT	1671227	AGATCATGCCATTGCCAGC	ACT
2019599 GAAAAGCATGGGCCGGGCA ACG 2116883 CATACTCACCAATATCTGCT ACT 2124090 GCTTTGTGTTCTTCTAGTC ACT 2163833 GCCAGCAATGCACGCGCAGT ACG 2217659 GTAACTTACCTAATGATAGAGG ACG 2304167 TGACTCCTTTGGACTGG ACG 2304168 CAGTTCGGTGAAGTGGTT ACT 2365593 GGTGTGAGCCACCACGCC ACG 2365721 AGACTCCCTCTCAAAATAA ACG 2569513 AGGGATAAGCATGAAACCACT ACG 2569514 GCGTGAGCCACCACGCC ACG 286414 GGGTGACAAAGTGAGACTC ACG 2886415 CACGCCTGGCTAAGCCT ACT 3745912 GGCTGGCAGGCCAGGTCAAC ACT	1671228	ACAGAAGTTAGCTGGGC	ACT
2116883 CATACTCACCAATATCTGCT ACT 2124090 GCTTTGTGTTCTTTCTAGTC ACT 2163833 GCCAGCAATGCACGCGCAGT ACG 2217659 GTAACTTACCTAATGATAGAGG ACG 2304167 TGACTCCTTTGGACTGG ACG 2304168 CAGTTCGGTGAAGTGGTT ACT 2365593 GGTGTGAGCCACCACGCC ACG 2365721 AGACTCCCTCTCAAAATAA ACG 2569513 AGGGATAAGCATGAAACCACT ACG 2569514 GCGTGAGCCACCACGCC ACG 2886414 GGGTGACAAAGTGAGACTC ACG 2886415 CACGCCTGGCTAAGCCT ACT 3745912 GGCTGGCAGGCCAGGTCAAC ACT	1869616	CTTCAACCTCCGCCTCCTGG	ACT
2124090 GCTTTGTGTTCTTTCTAGTC ACT 2163833 GCCAGCAATGCACGCGCAGT ACG 2217659 GTAACTTACCTAATGATAGAGG ACG 2304167 TGACTCCTTTGGACTGG ACG 2304168 CAGTTCGGTGAAGTGGTT ACT 2365593 GGTGTGAGCCACCACGCC ACG 2365721 AGACTCCCTCTCAAAATAA ACG 2569513 AGGGATAAGCATGAAACCACT ACG 2569514 GCGTGAGCCACCACGCC ACG 2886414 GGGTGACAAAGTGAGACTC ACG 2886415 CACGCCTGGCTAAGCCT ACT 3745912 GGCTGGCAGGCCAGGTCAAC ACT	2019599	GAAAAGCATGGGCCGGGCA	ACG
2163833 GCCAGCAATGCACGCGCAGT ACG 2217659 GTAACTTACCTAATGATAGAGG ACG 2304167 TGACTCCTTTGGACTGG ACG 2304168 CAGTTCGGTGAAGTGGTT ACT 2365593 GGTGTGAGCCACCACGCC ACG 2365721 AGACTCCCTCTCAAAATAA ACG 2569513 AGGGATAAGCATGAAACCACT ACG 2569514 GCGTGAGCCACCACGCC ACG 2886414 GGGTGACAAAGTGAGACTC ACG 2886415 CACGCCTGGCTAAGCCT ACT 3745912 GGCTGGCAGGCCAGGTCAAC ACT	2116883	CATACTCACCAATATCTGCT	ACT
2217659 GTAACTTACCTAATGATAGAGG ACG 2304167 TGACTCCTTTGGACTGG ACG 2304168 CAGTTCGGTGAAGTGGTT ACT 2365593 GGTGTGAGCCACCACGCC ACG 2365721 AGACTCCCTCTCAAAATAA ACG 2569513 AGGGATAAGCATGAAACCACT ACG 2569514 GCGTGAGCCACCACGCC ACG 2886414 GGGTGACAAAGTGAGACTC ACG 2886415 CACGCCTGGCTAAGCCT ACT 3745912 GGCTGGCAGGCCAGGTCAAC ACT	2124090	GCTTTGTGTTCTTTCTAGTC	ACT
2304167 TGACTCCTTTGGACTGG ACG 2304168 CAGTTCGGTGAAGTGGTT ACT 2365593 GGTGTGAGCCACCACGCC ACG 2365721 AGACTCCCTCTCAAAATAA ACG 2569513 AGGGATAAGCATGAAACCACT ACG 2569514 GCGTGAGCCACCACGCC ACG 2886414 GGGTGACAAAGTGAGACTC ACG 2886415 CACGCCTGGCTAAGCCT ACT 3745912 GGCTGGCAGGCCAGGTCAAC ACT	2163833	GCCAGCAATGCACGCGCAGT	ACG
2304168 CAGTTCGGTGAAGTGGTT ACT 2365593 GGTGTGAGCCACCACGCC ACG 2365721 AGACTCCCTCTCAAAATAA ACG 2569513 AGGGATAAGCATGAAACCACT ACG 2569514 GCGTGAGCCACCACGCC ACG 2886414 GGGTGACAAAGTGAGACTC ACG 2886415 CACGCCTGGCTAAGCCT ACT 3745912 GGCTGGCAGGCCAGGTCAAC ACT	2217659	GTAACTTACCTAATGATAGAGG	ACG
2365593 GGTGTGAGCCACCACGCC ACG 2365721 AGACTCCCTCTCAAAATAA ACG 2569513 AGGGATAAGCATGAAACCACT ACG 2569514 GCGTGAGCCACCACGCC ACG 2886414 GGGTGACAAAGTGAGACTC ACG 2886415 CACGCCTGGCTAAGCCT ACT 3745912 GGCTGGCAGGCCAGGTCAAC ACT	2304167	TGACTCCTTTGGACTGG	ACG
2365721 AGACTCCCTCTCAAAATAA ACG 2569513 AGGGATAAGCATGAAACCACT ACG 2569514 GCGTGAGCCACCACGCC ACG 2886414 GGGTGACAAAGTGAGACTC ACG 2886415 CACGCCTGGCTAAGCCT ACT 3745912 GGCTGGCAGGCCAGGTCAAC ACT	2304168	CAGTTCGGTGAAGTGGTT	ACT
2569513 AGGGATAAGCATGAAACCACT ACG 2569514 GCGTGAGCCACCACGCC ACG 2886414 GGGTGACAAAGTGAGACTC ACG 2886415 CACGCCTGGCTAAGCCT ACT 3745912 GGCTGGCAGGCCAGGTCAAC ACT	2365593	GGTGTGAGCCACCACGCC	ACG
2569514 GCGTGAGCCACCACGCC ACG 2886414 GGGTGACAAAGTGAGACTC ACG 2886415 CACGCCTGGCTAAGCCT ACT 3745912 GGCTGGCAGGCCAGGTCAAC ACT	2365721	AGACTCCCTCTCAAAATAA	ACG
2886414 GGGTGACAAAGTGAGACTC ACG 2886415 CACGCCTGGCTAAGCCT ACT 3745912 GGCTGGCAGGCCAGGTCAAC ACT	2569513	AGGGATAAGCATGAAACCACT	ACG
2886415 CACGCCTGGCTAAGCCT ACT 3745912 GGCTGGCAGGCCAGGTCAAC ACT	2569514	GCGTGAGCCACCACGCC	ACG
3745912 GGCTGGCAGGCCAGGTCAAC ACT	2886414	GGGTGACAAAGTGAGACTC	ACG
	2886415	CACGCCTGGCTAAGCCT	ACT
3786863 GTGCTGGGATTACAGGC ACT	3745912	GGCTGGCAGGCCAGGTCAAC	ACT
	3786863	GTGCTGGGATTACAGGC	ACT

Please delete paragraph [0259] and replace it with the following paragraph:

[0259] The methods used to verify and genotype the proximal SNP of Table 13 are the same methods described in Examples 1 and 2 herein. The PCR primers and extend primers used in these assays are provided in Table 11 and Table 12, respectively.

TABLE 11

dbSNP rs#	First PCR primer (SEQ ID NO: 403)	Second PCR primer (SEQ ID NO: 404)
1654416	ACGTTGGATGTCTGCTGAGCATGAAATGCC	ACGTTGGATGCTGAACTGACCGTCTCATTC

TABLE 12

dbSNP	Extend	Term
rs#	Primer (SEQ ID NO: 405)	Mix
1654416	TGACCGTCTCATTCACAAAC	

Please delete paragraph [0262] and replace it with the following paragraph:

[0262] The methods used to verify and allelotype the proximal SNPs of Table 14 are the same methods described in Examples 1 and 2 herein. The PCR primers and extend primers used in these assays are provided in Table 15 and Table 16, respectively. The methods used to verify and allelotype the proximal SNPs of Table 14 are the same methods described in Examples 1 and 2 herein. The PCR primers and extend primers used in these assays are provided in Table 15 and Table 16, respectively.

TABLE 15

dbSNP rs#	Forward PCR primer (SEQ ID NOS 406-476)	Reverse PCR primer (SEQ ID NOS 477-547)
LAMA4_SNP5	ACGTTGGATGACAGTTCTTGGCTATCCTGG	ACGTTGGATGACTGGCCAGTGTAGGAATTG
LAMA4_SNP6	ACGTTGGATGGAAAGGGATTGACTCAGGAG	ACGTTGGATGCTTCCTTCACCTGAAGATGG
LAMA4_SNP4	ACGTTGGATGTTGAAGGACTGATCTATGGG	ACGTTGGATGAAAGCAACAGACAAGGCAAG
LAMA4_SNP1	ACGTTGGATGCAGACTGGAAATGCGCAATG	ACGTTGGATGCGTATCTTCAAGATGCACAG
1050348	ACGTTGGATGTGTTCATGTCTTCGGCATCC	ACGTTGGATGCAGCTGGATGACTACAATGC
LAMA4_SNP2	ACGTTGGATGAGGAATGCTTACAACGGAGG	ACGTTGGATGAACTCCCTTCATCCTTCCTC
744006	ACGTTGGATGTTGCCTTGAAGGTAGGCATG	ACGTTGGATGGGGTTAGCAGCTTAACTTTC
763247	ACGTTGGATGCCGGCCAAGACCAATACATC	ACGTTGGATGTGCAGACATGCACTATTCTC
764071	ACGTTGGATGCCACTTGGAAAGATTCAAGG	ACGTTGGATGTATTGTGACTTCTGCAGAAC

764587	ACGTTGGATGCAACATAGACCAGAAGTGGG	ACGTTGGATGTTCACATACGGAAGGCCTTG
969138	ACGTTGGATGACTGGACCAAGGTAGATCAC	ACGTTGGATGCTCAGGCTAATCTCTCTAGG
971402	ACGTTGGATGCCACTTTTCTGTGGAAATATC	ACGTTGGATGCAAGTTAATGAGTTTCTCCC
971405	ACGTTGGATGAAACAGTGCTTTTGAAGGAG	ACGTTGGATGCTATCTCCAAAGGGTAACAG
1050348	ACGTTGGATGCAGCTGGATGACTACAATGC	ACGTTGGATGTGTTCATGTCTTCGGCATCC
1050349	ACGTTGGATGCTATGATTTTGGATTCAGCG	ACGTTGGATGACCTCATGGTATTTTGCATC
1158747	ACGTTGGATGTTGAAGGACTGATCTATGGG	ACGTTGGATGAAAGCAACAGACAAGGCAAG
1418499	ACGTTGGATGACCATAGGGAACTAGAAATC	ACGTTGGATGCTTTAAGATAGATTCCCAGGG
1480646	ACGTTGGATGCAGTGTCTCTTCCTTTCCAG	ACGTTGGATGCAAATTTCCACGAGCCTGAG
1894681	ACGTTGGATGTGGGATTCCCCTAAAGGATG	ACGTTGGATGAAGATCAGCAGCACCAAAGG
2032565	ACGTTGGATGAAAGAGCAACTGAAGGACCC	ACGTTGGATGTAAATTGGAACATCAACAGG
2032566	ACGTTGGATGTAAATTGGAACATCAACAGG	ACGTTGGATGAAAGAGCAACTGAAGGACCC
2032567	ACGTTGGATGCGTATCTTCAAGATGCACAG	ACGTTGGATGAGACTGGAAATGCGCAATGG
2032568	ACGTTGGATGACTCGCATAACAGATGTTCC	ACGTTGGATGTAACCATTGCGCATTTCCAG
2051649	ACGTTGGATGACCTGCTGAAAACCAACACC	ACGTTGGATGGGAGAGGAGAACCCTGGAC
2068770	ACGTTGGATGCACTTCACGTACTTCACTGG	ACGTTGGATGAGTTTGCTCCTATGTGGCTC
2072019	ACGTTGGATGAGGTCCACAGAAGATGTTAG	ACGTTGGATGCACAACGGTCATTTGAACAC
2072020	ACGTTGGATGAAGTCCTGTTGTCTGCAAGG	ACGTTGGATGCAGTTGTCTTAGCACACAGG
2072022	ACGTTGGATGCAAAGAAGAAGATGTAGTGG	ACGTTGGATGCGAAATCTGGTCCTATGAAG
2072026	ACGTTGGATGTCCTATCACCATCACACTAC	ACGTTGGATGCAGCATCAAACAGAATAGGC
2072029	ACGTTGGATGTCCTTGCAGACTGATACTCC	ACGTTGGATGTCACTCACTCCTTGCTAAGC
2157544	ACGTTGGATGCATATGTAGTAGGAATGAGGG	ACGTTGGATGTGAGGCTCAAAGGGATTAGG
2157545	ACGTTGGATGTCTGGTCAACCACATAGATC	ACGTTGGATGTGTTCTACTGCAGCTCCAAG
2157546	ACGTTGGATGTCCACTTGTACAGAATGGAG	ACGTTGGATGCATTTACTCAGTGCCAGGTC
2157547	ACGTTGGATGCCATACCATTTACTTCTGCC	ACGTTGGATGAGGCAAGTACACATACAATG
2157550	ACGTTGGATGCACACACACATTTTAATTGCC	ACGTTGGATGTTGTTCAGAATTACATGATG
2213838	ACGTTGGATGAAAGGACTTGAGGGTGATTG	ACGTTGGATGGCAACAAACAGTGTTCCAGC
2213839	ACGTTGGATGAGTCACAGTTCAGTCCCAAC	ACGTTGGATGGGGCAATTTTCTAGTCCAGC
2213840	ACGTTGGATGCTTTCGCACAAGGCTCTATC	ACGTTGGATGAAGTCTGTGTTTAAGCCCCC
2227237	ACGTTGGATGGATGTCTCTAAGTTGAAATGC	ACGTTGGATGATATCAATCACCCTCAAGTC
2237238	ACGTTGGATGCAGAGGCTGAAGGAACATAC	ACGTTGGATGTCTGTAATCCCAGGACCCTA
2237241	ACGTTGGATGTCAGCAGGGCTCTATCTAAG	ACGTTGGATGCCAAGCAGTATTGCTAATGG
2237242	ACGTTGGATGCCTCACCATTGTGTTTAGGC	ACGTTGGATGTGACTATTTCCGCTTGGCTC
2237244	ACGTTGGATGGAGAAAAATAGACTCGGCCC	ACGTTGGATGCACAGACGCAGGATTTGGAT
2237247	ACGTTGGATGCTGCTTCTCCAGTAATGTTG	ACGTTGGATGGTGTTAGTAACACTGATGCC
2237248	ACGTTGGATGCCCTCCCCAGATATCATTAG	ACGTTGGATGCATATCCACAGCCTAATCAC
2237249	ACGTTGGATGAAATGCTTCCTACTGCAATC	ACGTTGGATGTGGAGAGTTGTGGTTGATGG
2239849	ACGTTGGATGGACATCAGATCAGACAGCAC	ACGTTGGATGACTTTCTGGCATTGACTGGG
2239850	ACGTTGGATGGCCCAGGAAAAATTAATTCAC	ACGTTGGATGGCAGTACGGATTAGCATGAG
2269646	ACGTTGGATGTCACCTCACTTTTGAAGAGC	ACGTTGGATGTCTGGTTAGGCTTCAGTTAG
2277084	ACGTTGGATGGAGGGTAAAAATGACAGCAG	ACGTTGGATGTTTTGCTTGGTGTTTAGCAG
2282853	ACGTTGGATGTCTTGACCTTCCTGGTTTTC	ACGTTGGATGTATCAGAGCTAGAAGAAACC
2282854	ACGTTGGATGTAGCCAGTGGTTAAGAAAGC	ACGTTGGATGTTCTCATGTTGGGGAGACAC
2301512	ACGTTGGATGATCTGAGTGGTTTCAGGAGG	ACGTTGGATGACCTGTTGGAACACATGAAG
2301513	ACGTTGGATGCTGGCGGGTAGTGTCTTCAT	ACGTTGGATGCTTTGAAATTGTTCTTGTCC
2345808	ACGTTGGATGTTCTGGGATTTAAAGGAGGC	ACGTTGGATGCCAAACATTTCTTGTTGGAC
3734286	ACGTTGGATGACCTTACACTCCAGTGAATC	ACGTTGGATGGCCGTTAAGCAACTACAAGC
3734287	ACGTTGGATGCAGTGGAGAAGATGAAACCC	ACGTTGGATGCCCACTTCTGGTCTATGTTG
3752577	ACGTTGGATGCATGGCTGAGGTTACTTAGG	ACGTTGGATGGAATGCGTCAGGGATTTATG
	· · · · · · · · · · · · · · · · · · ·	

3777925	ACGTTGGATGCTACAAGTCTAACAGTCAGAG	ACGTTGGATGTTACAGAGCAAGGTCTGAGG
3777926	ACGTTGGATGGTGAGTACCATCCCTTTTGC	ACGTTGGATGCTGTTAAACTGCCTCAGACC
3777927	ACGTTGGATGAAACGAATGCTTGAGAGCAG	ACGTTGGATGGTCCTGATTTATGAGCTCCC
3777928	ACGTTGGATGTTCACACGTAGACCCTGTTG	ACGTTGGATGTCAGGAGTTGAGCAAGCTAG
3777929	ACGTTGGATGGCTGTCTTTGGGATTAAAT	ACGTTGGATGTTCATAAAGAAGTGGAGAGC
3777932	ACGTTGGATGTCCCAGACCTTAAGATTCCC	ACGTTGGATGTATTAGGCTCTTTGGCCGAC
3777934	ACGTTGGATGCAAGATCCAGATGGTGAGGG	ACGTTGGATGCAAGGTCAGAGTGTCACTGG
3777941	ACGTTGGATGGCTTCCTGAGATTATATTGAC	ACGTTGGATGCTCCATTCCAAATTCCTTTC
3777942	ACGTTGGATGTCATGACAAATCATGACTAG	ACGTTGGATGTCAGATACAAGTGAAGGTAG
3798357	ACGTTGGATGTCCCAATTCAGGAAATGGTG	ACGTTGGATGTGCTTGGTATACCATGCCTG
3798359	ACGTTGGATGTTCCTCAGCACACAGCCCCA	ACGTTGGATGATGAACCTTACACAGGCCAG
3822941	ACGTTGGATGTATAATAAACTGATAGTTGC	ACGTTGGATGCTCTGTACTTAGGACACACG
3948760	ACGTTGGATGTCCACTTGTACAGAATGGAG	ACGTTGGATGTCCCACACTCAAAACTTTGC

TABLE 16

dbSNP rs#	Extend Primer <u>(SEQ ID NOS 548-618)</u>	Term Mix
LAMA4_SNP5	ATTGCTTACGCAACACCAC	ACG
LAMA4_SNP6	AGATGGAGAGAATGCCAC	CGT
LAMA4_SNP4	GCAAGTGGGCATTCGACCA	CGT
LAMA4_SNP1	CTTCAAGATGCACAGGGCCAC	ACG
1050348	CACTTGACCAGGCCCTTAAC	ACG
LAMA4_SNP2	GGCCCGCCTGCATCTGTG	ACG
744006	CTTTCTCTCTTTCCAGG	ACG
763247	CTTTAATCCCCCACACT	ACT
764071	AGAACATATATGTTGCATTTTTT	ACT
764587	GAAGGCCTTGCCTGTTA	ACT
969138	AGGAAGAGAATCTGATAGCC	ACT
971402	AGTTTCTCCCACTTACC	ACT
971405	AGGGTAACAGAATGATTAAAA	CGT
1050348	TTCGGCATCCCTGACAT	ACT
1050349	CGTATCTTCAAGATGCACA	ACT
1158747	GCAAGTGGGCATTCGACCA	CGT
1418499	GGGCAGAATTACTGAATCAAG	ACT
1480646	CAGCAGACTCTGATGTGGC	ACG
1894681	GGGAGCATCTTTTGAGC	ACT
2032565	CAACAGGAAAAATACATCCA	CGT
2032566	CAACCCTAGGAAAACATTT	ACT
2032567	TTCTATGATTTTGGATTCAGC	ACT
2032568	ACATACTCTGAGGAGAGAAAG	ACT
2051649	GAACCCTGGACAAGAAT	ACT
2068770	ATGTGGCTCAAACATCCGAA	ACT
2072019	TTTGAACACTACAGTTTCTGTTAT	ACT
2072020	AAACAATCCATTTAACATACCTA	ACG

2072022	GCAAATGAATTCTGGGA	ACT
2072026	TGAAAGTCTTTGAGGTGTT	ACG
2072029	CCTGGCAATGATCAACCCCC	ACT
2157544	CTAAATATTAGCAGACTGAAATAC	ACT
2157545	GCTGGCATAAATGAAATTG	ACG
2157546	GTGCCAGGTCCCACACT	ACT
2157547	GTACACATACAATGATTTTACTC	ACT
2157550	TTACATGATGAATATTATGGAAGT	ACT
2213838	TTCCAGCATGATTCTAAGACA	ACT
2213839	CAACTTGAGATACAGTAAAAATT	ACG
2213840	TGAAATGAATTCTCCAATAGAC	ACG
2227237	ACCCTCAAGTCCTTTTG	ACG
2237238	TCCCAGGACCCTAAAAAAGT	CGT
2237241	CAGTATTGCTAATGGGTGTTC	ACT
2237242	TGTCTCTAGGGCACTACATATC	ACT
2237244	GAAATAATGCTTCAGGGG	ACT
2237247	ATGCCTTCTAATGCATTCATTTTA	ACG
2237248	CCTAATCACATAAACCAGGAA	ACG
2237249	GAAAACAAGAGAGGGAAG	ACT
2239849	TGTGACTCCTCATGCTAATC	ACG
2239850	CCAGTCAATGCCAGAAA	ACT
2269646	CAGTTAGACTGAAACGCACA	ACT
2277084	TGTGTCATTTAAATCCTTCA	ACT
2282853	GAGCTAGAAGAACCTGAAAG	ACT
2282854	GTTGGTGTCCAAATGGCA	ACT
2301512	ACATGAAGACACTACCC	ACT_
2301513	TGTTCTTGTCCAAAATTACCT	ACT
2345808	GACATTTAGGTTATTTCCAAATTT	ACT
3734286	CATCAGAGAGAATTGAAGT	ACT
3734287	GGAATTCAGGCATACAC	ACG
3752577	AGAAATAGATGGAGCCAAAAG	ACG
3777925	GGATGGGACTGAAACTC	ACT
3777926	CTCTGTAATTTTTCATGTATGATA	ACT
3777927	ATGAGCTCCCTTCACTC	ACG
3777928	TGAGCAAGCTAGAGAGTA	CGT
3777929	AAGTGGAGAGCATTTACAT	ACT
3777932	TTTGGCCGACTGAAATG	ACT
3777934	GGTCAGAGTGTCACTGGGCTACA	ACT
3777941	TCCCAAATTTCCTTTTCA	ACG
3777942	ACAAGTGAAGGTAGTATTGT	CGT
3798357	GCCTGGCATCTGCTAATC	ACT_
3798359	GCAAAGGCAGAGACTAT	ACT
3822941	ACACACGATGTTTCTCCAG	ACG
3948760	ACAGTTTTATGAGACAGGTA	ACT

Please delete paragraph [0268] and replace it with the following paragraph:

[0268] The methods used to verify and allelotype the sixty-three proximal SNPs of Table 18 are the same methods described in Examples 1 and 2 herein. The PCR primers and extend primers used in these assays are provided in Table 19 and Table 20, respectively.

TABLE 19

dbSNP rs#	Forward PCR primer (SEQ ID NOS 871-973)	Reverse PCR primer (SEQ ID NOS 974-1076)
		ACGTTGGATGCCAATTGTGTCAAACATTTAAT
54144	ACGTTGGATGAGCAGCCATCACATGATCTG	GAA
183535	ACGTTGGATGTGGTCTAAGTCCTGCACAAG	ACGTTGGATGGACAGAAAGAGTGTGCAGTC
236104	ACGTTGGATGCTCCCTGAACTTCCCATTTC	ACGTTGGATGCAGGGAGCTTACTACAAAGC
236105	ACGTTGGATGGGTAGCCACATTTGACACAG	ACGTTGGATGAAGTGGCCTGGAAACCAATG
236113	ACGTTGGATGGCTAATACATCCTAAAGGAAC	ACGTTGGATGCTTTATTGGAAATCTGTTCG
236119	ACGTTGGATGTTTCTTCTTGTCTCACAGGC	ACGTTGGATGCTGTAGATTTTCCTTTTGGC
236120	ACGTTGGATGCAGGATAATGATCATCCCTG	ACGTTGGATGACTGGCACAATTAGTGTCTG
236122	ACGTTGGATGTAGCTATCCCATTGTTGAGG	ACGTTGGATGGCTAAAGTCTGAAAACACTAG
236143	ACGTTGGATGCCTACCCCAAATAGGTAAAG	ACGTTGGATGAGGAAGTAAGTTTTGGGAGG
236145	ACGTTGGATGAGAATGTGAGCAAGGGATGC	ACGTTGGATGAATGGCACAGCTATCCTCAG
236146	ACGTTGGATGGTAAATCTGTATCTCCGCCC	ACGTTGGATGGACTTGATTACGTGACCTGG
236149	ACGTTGGATGCCAATGATCAAACTGAAATCG	ACGTTGGATGGGACTGGATTAGATGAATTC
236160	ACGTTGGATGCACCCACAGCTATCTGAGTT	ACGTTGGATGTCCAAAAGGAGTGGGTAGAG
236162	ACGTTGGATGAATGGAGTGTTTGCATGTTG	ACGTTGGATGCATGGATTTTTAGGACATGCG
236163	ACGTTGGATGGCCAAAAATAGCCTTTTCTC	ACGTTGGATGAAACACATGCAAACACTCC
236164	ACGTTGGATGTTGCAAGCTGGTGTCACACA	ACGTTGGATGAGACCAGCCACTACTGATTC
236166	ACGTTGGATGCTCCTGTCATAGAATAGGCC	ACGTTGGATGGCATAGCACATGCTATTTGG
236167	ACGTTGGATGATCAAAGTCTTGTGCAGGAC	ACGTTGGATGGCACTTTAGGGACATTTGAC
236176	ACGTTGGATGGCATAGATAGCTTAATCATGG	ACGTTGGATGAAACCAATAGAAGCAGGTTG
236177	ACGTTGGATGCATTTGAGGATCGGAGTGAG	ACGTTGGATGCCCTGTGTCTGCAAATTTGG
236180	ACGTTGGATGCCTAGCACTTGGGAATTAGG	ACGTTGGATGGATGCGTGAAATAGATGCTC
236182	ACGTTGGATGCTCTCTAGTTCCTTTGTTGC	ACGTTGGATGATTTCAAAAGTGGTCTCCAC
236183	ACGTTGGATGTAAAAGAGAAATCCCACAGG	ACGTTGGATGCTCAGCAGATGTTAGTTTTC
236184	ACGTTGGATGCTAGGGACCCAGCAAATAAC	ACGTTGGATGACCATCTGAGGGAAATCCTG
379418	ACGTTGGATGTCTGGCCTCTAAGCTAAAGG	ACGTTGGATGCAGTGGTGTTGATAGATGGG
400735	ACGTTGGATGACCTTCTCAGGTTCACGTTC	ACGTTGGATGAAGGGCACCATGCCATTAAC
409035	ACGTTGGATGTGCTATGGGTATGCAAGGTG	ACGTTGGATGGGTTGTTGAAGGAGCGAGAG
440005	ACGTTGGATGATGGCTCTAAAAAGCTGTCC	ACGTTGGATGCAGCCTTCTTCCTGATACAG
446614	ACGTTGGATGTAAAGCCCAGGGCTAAAGAC	ACGTTGGATGAGAAGGAGGAGAAGGAG
451417	ACGTTGGATGCCAGAGTCATCGTTATCACC	ACGTTGGATGCCTCACTAAGGATTCAACCC
454422	ACGTTGGATGCAGCTTTTGAGGCACTTTCC	ACGTTGGATGAGCACCTTGCATACCCATAG

	·	
500277	ACGTTGGATGAGTTTCCCTACGTCTCTCTC	ACGTTGGATGAGTAACTCTAGCCTCTGCTC
540717	ACGTTGGATGCATCCAAAACCCAACAAATCC	ACGTTGGATGAGAGAGGTGTGTGACTTTTC
546106	ACGTTGGATGTTATAGCACTGATGGGCTCC	ACGTTGGATGCTGTGACATACTTTTCCAGG
571039	ACGTTGGATGATTCCTGTAGCAGGCAACTG	ACGTTGGATGGCTAGCTCTACTCTCTCTC
1039542	ACGTTGGATGTGAGGTTCTGTCTGAACACC	ACGTTGGATGTGGCTGCAATGGCTAACTTC
1039543	ACGTTGGATGATCTGACTCAGAAGAAGAGC	ACGTTGGATGGGCATTAATGGAGGTTATGC
1343180	ACGTTGGATGAGATGGCAACAGCACAG	ACGTTGGATGCCAACAGCAGCTTCACAATC
CHGB_SNP2	ACGTTGGATGAAATGGTATGTTTGTGTTCC	ACGTTGGATGTAATTTTTCCCCCCCAAATC
rs384578	ACGTTGGATGAAATGGTATGTTTGTGTTCC	ACGTTGGATGTAATTTTTCCCCCCCAAATC
rs742710	ACGTTGGATGAGAAAGTGAGGAAGAGAGGG	ACGTTGGATGATGAAATAGGCACGTGGCTC
rs742711	ACGTTGGATGATGAAATAGGCACGTGGCTC	ACGTTGGATGAGAAAGTGAGGAAGAGAGGG
rs881118	ACGTTGGATGTATAGCTGAAGCCTGCTTTC	ACGTTGGATGCAGTGAAGAGAAACACCTTG
rs910122	ACGTTGGATGAAGGTGTTTCTCTTCACTGC	ACGTTGGATGGGAGGGAGAACTATCAAA
CHGB_SNP1	ACGTTGGATGTCACTCTGAGGTCTTGGAGC	ACGTTGGATGTAAAGGGTTATCCAGGCGTC
180477	ACGTTGGATGGGAAGTAATTCTCTGGGCTG	ACGTTGGATGAAGTGATCCTCCCACCTCAG
236102	ACGTTGGATGCAGCCTGTTCTCTCTGAAAC	ACGTTGGATGGGATGCAAGAGGTTGTAGAG
236103	ACGTTGGATGCCTGTTTAAATCGTGGCTCC	ACGTTGGATGAAACATAAGGAAGCTGAGGC
236106	ACGTTGGATGCAAGCCTTTGCAGCTCTATC	ACGTTGGATGCCTCATAAGGGCCTTTGTAC
236107	ACGTTGGATGGAAGTTTACGTAAACTCTAG	ACGTTGGATGGTGTGTGGCTTATTGTAGAG
236108	ACGTTGGATGGTATTTACTGTTGAACCCAG	ACGTTGGATGATGTGGGTAAGTTGTGCACC
236109	·ACGTTGGATGAGATTACAGGCACTAGCCAC	ACGTTGGATGTCTGGGCAACATGGTGAAAC
236110	ACGTTGGATGATCGATCCAATGTTGACTGC	ACGTTGGATGTTTCAGAACAAACCCCACAG
236111	ACGTTGGATGTTCAGGAAGCAGCAACCATC	ACGTTGGATGTATGCTGTGACCTCTCCAAC
236112	ACGTTGGATGAACGAGGTCAGGAGATCAAG	ACGTTGGATGCACGCCCGGCTAATTTTTC
236114	ACGTTGGATGGAACCAAGGAAGTCTGACTC	ACGTTGGATGAAAGCTACCAGTCATGTGCC
236115	ACGTTGGATGATCAAAGTCCATACTGCAGG	ACGTTGGATGTATGATCGTAGGCACTGGAG
236116	ACGTTGGATGTGTTGTATTACCTGACCCTG	ACGTTGGATGAAGCAAACCACTGAGTGTCC
236117	ACGTTGGATGCAATGGTGTGATCTTGCCTC	ACGTTGGATGATTAGCCAAGTGTGGCAGTG
236118	ACGTTGGATGGGTTGAGTATCCCTAATCTG	ACGTTGGATGCTTTCAGTGTCGTGTCAGGG
236121	ACGTTGGATGCAAGCTATGTCACAGTTTAAG	ACGTTGGATGAGTCTTTGCCCTTAATGTGG
236123	ACGTTGGATGATAATAAATTTAGACTTCAC	ACGTTGGATGAAAATACTGGTGCGGCCAGA
236124	ACGTTGGATGGAATTTTGTTTGGCTCACGG	ACGTTGGATGATTGCTGCTGGAAGCTTACC
236125	ACGTTGGATGCCATGCCTGAGTTATTTGC	ACGTTGGATGATGGAGAAAGTAGATAGTAG
236148	ACGTTGGATGTAAGCCCAAGTGCTGTTGAG	ACGTTGGATGCTCAGAAGTCTGATGTGTATC
236151	ACGTTGGATGTTGGCCTTTAGACTCCTGGG	ACGTTGGATGAGAAGACACATAGCCGAGAG
236152	ACGTTGGATGAATAAAGGGTTATCCAGGCG	ACGTTGGATGTGGAGCCCTGTATTCTTCAC
236154	ACGTTGGATGTTCTGACAAGTTCCTGGCTG	ACGTTGGATGGCTGCATTAGTCAACCTACC
236155	ACGTTGGATGGGTAGGTTGACTAATGCAGC	ACGTTGGATGTGAGGTCCCGAACCAATTTC
236158	ACGTTGGATGAAACTCCTGACCTCGTGATC	ACGTTGGATGCTCCTTAAGAAGATAGAGGC
236159	ACGTTGGATGGTCTCAAACTCCTGACCTCG	ACGTTGGATGAAGAAGATAGAGGCAGCTGG
236161	ACGTTGGATGGATGTTGCCTCTAGGCTAGT	ACGTTGGATGCACCATCTGACCTGTGCTAC
236165	ACGTTGGATGAAAATTAGCCATGCGTGGTG	ACGTTGGATGTTCAAGCGGTTCTCCTGCCT
236168	ACGTTGGATGTCTATGTCTCCACTTGCATG	ACGTTGGATGACACATTTGCACACACACAC
236169	ACGTTGGATGGTGACTAGAATTTTTGTGTAC	ACGTTGGATGGTGTGCAAATGTGTATCC
236171	ACGTTGGATGAACCTCCCACTTTGGCTTTC	ACGTTGGATGGGTCCATTTAAAGCCTGGTG
236173	ACGTTGGATGATCAACCTGCACCACCAATC	ACGTTGGATGGCTAAGATGGAAGTTGAAGTG
236175	ACGTTGGATGTTCTCCATCACTGCATCAAG	ACGTTGGATGGTTATAGCCTGTATCGCAGC
236179	ACGTTGGATGCTAAATAACAGGTTTGACTC	ACGTTGGATGGAACATTGAGAGTATCTTAT
236181	ACGTTGGATGGTGAACATGTCTTTTCTGTAC	ACGTTGGATGGGTAGAACCACTGTTTTTCG
230101	AUDITOURIOGIONALATOTOTITIOIDIAO	7.55.155.11110

236185 ACGTTGGATGGGGTCACTTGAATTCAGGAG ACGTTGGATGACTGCACCACTGCCTCTTG 236187 ACGTTGGATGTAGTGAAACTCTGTCTCTGC ACGTTGGATGACCCAACCACCTTTAACC 236189 ACGTTGGATGTGGATTTACAGAAAAACTGC ACGTTGGATGCTGTGAGACACTAGGGATAC 364652 ACGTTGGATGTTTCTGCTGGGCTGTGATAG ACGTTGGATGGGGAAATGCTCAGCATGTAC 394604 ACGTTGGATGTATTTTGGGATGGTGTGGGC ACGTTGGATGGAACCAGGTCTTCCTTGATG 403727 ACGTTGGATGTCACTTGAACCCAGGAGATG ACGTTGGATGGAACCAGGTCTTCCTTGATG 403727 ACGTTGGATGTCACTTGAACCCAGGAGATG ACGTTGGATGGTTTTGAGACAGAGGTTTCGC 446658 ACGTTGGATGTCACTGAGTTCAACTCCTTC ACGTTGGATGGTTCACCTTCG 451571 ACGTTGGATGTCACTGAGTTCACTCTTG ACGTTGGATGAAAGTAATGGCACACTGGAGG 452749 ACGTTGGATGTCCTACTCCAGTATGACCTC ACGTTGGATGGAAGTAATGGCACACCCTAATAC 454328 ACGTTGGATGTCCACTACTACAACACTCCTC ACGTTGGATGGAAGTCCCAACCCCTAATAC 454328 ACGTTGGATGGCAAACTGGTGCATCAGAG ACGTTGGATGCCTCTGTTATTCATATCGCC 742710 ACGTTGGATGGGCACATGGATATGGTGAAG ACGTTGGATGACCTCGTGATGGTGCCC 881118 ACGTTGGATGGACAACTGGATATGGTGAAG ACGTTGGATGACCTCGCTGATGATGCTCCC 881118 ACGTTGGATGGATGATAGCTGAAGACACTGCTTC ACGTTGGATGACACGCCATTCTGAGAAGACACC 910122 ACGTTGGATGGATGATAGCTGAAGCCTGCTTTC ACGTTGGATGACACGCCATTCTGAGAAGAC 1994095 ACGTTGGATGATACTAATGTCAGTGGTAGAG 1005517 ACGTTGGATGATACTAATGTCAGTGGTAGAG 1094095 ACGTTGGATGATCCAACTTCCGC ACGTTGGATGGAAACCCCTTGATTGGC 2206817 ACGTTGGATGATCCAACTTCCGC ACGTTGGATGACACCCCATTCTGAGAAAC 1994095 ACGTTGGATGATCCAACTTCCGC ACGTTGGATGACACCCCATTCTGATTGGC 2206817 ACGTTGGATGATCCAACTCCGC ACGTTGGATGAAACCAGTTACTAACTGTAG 2266339 ACGTTGGATGATCCAGGATGTTATACCC ACGTTGGATGAAACCAGTTACTAACTGTAG 226680 ACGTTGGATGATCCAACTCCTGCGTAGAGAAACCAGTTACAACCAGCCAACTCCTTGATTGGC 2206817 ACGTTGGATGATCCAACTTCCTGC ACGTTGGATGAAACCAGTTACTAACTGTAG 226680 ACGTTGGATGATCCAACTTCCTGC ACGTTGGATGAACACCAGTTACTAACTGTAG 226680 ACGTTGGATGATCCAACTCCTTCTCCTGG ACGTTGGATGAACACTGACTAACTGTGCC 2206817 ACGTTGGATGATCCAACTACCAGAATTACCTGTGCT 2423131 ACGTTGGATGAGACAAACCCAGAAACCAATCACTGTGTC 2423131 ACGTTGGATGATGCCTGCCTTTACGAGAATG ACGTTGGATGCAACATCACTGTGTC 2423131 ACGTTGGATGATGCCAAAACCCATTACAGAGATTCTGAAGACATTCTGAACAACCAGAGATTCTGAACAACACAGAGATTCTGAAGAGATTCTGAAGACATTGAACACAGAGATTCT			
236189 ACGTTGGATGTGGATTTACAGAAAAACTGC ACGTTGGATGCTGTGAGACACTAGGGATAC 364652 ACGTTGGATGTTCTGCTGGGCTGTGATAG ACGTTGGATGGGGAAATGCTCAGCATGTAC 394604 ACGTTGGATGTATTTTGGGATGGTGTGGGC ACGTTGGATGGAACCAGGTCTTCCTTGATG 403727 ACGTTGGATGTCACTTGAACCCAGGAGATG ACGTTGGATGGTTTTGAGACAGAGTTTCGC 446658 ACGTTGGATGTCACTCACTCCTTC ACGTTGGATGGTTCCTGCTTTACCACTTCG 451571 ACGTTGGATGTCCTCTCTGATGCTCTCTTC ACGTTGGATGATACTGCACCTTGAGG 452749 ACGTTGGATGTCCTACTCCAGTATGACCTC ACGTTGGATGAAGTACCCAACCCCTAATAC 454328 ACGTTGGATGTCCAACTCGTGCATCAGAG ACGTTGGATGCCTGGATGTTTCATATCGCC 742710 ACGTTGGATGGCAAACTGGTGCATCAGAG ACGTTGGATGCCTCTGTGATGGTCCC 742711 ACGTTGGATGGGCACATGGATATGGTGAAG ACGTTGGATGACCTCTGTGATGGTTCCC 881118 ACGTTGGATGGTAAGCTGAAGCCTGCTTTC ACGTTGGATGAAAATAGGCACGTGGCTCCCC 881118 ACGTTGGATGATATAGCTGAAGCCTGCTTTC ACGTTGGATGAAAACACCC 910122 ACGTTGGATGATCAATGTCACTGCTATCT ACGTTGGATGACACGCCATTCTGAGAAGAG 1005517 ACGTTGGATGATCAATGTCAGTGGTAGAG ACGTTGGATGAAACACCCCCTGAAAAC 1394095 ACGTTGGATGACCAAACCCAGTGAAGAG ACGTTGGATGAAAACCCCCTTGAAAAC 1394095 ACGTTGGATGACCAGAAACCCAGTGAAGAG ACGTTGGATGAAAACCAGTTACTAACTGTAG 2268339 ACGTTGGATGACCAGAAACCCAGTGAAGTAG ACGTTGGATGAAACCAGTTACTAACTGTAG 2268339 ACGTTGGATGACAAACCCAGTGAAGTAG ACGTTGGATGAAACCAGTTAACTGTAG 2268339 ACGTTGGATGAAGAACCCAGTGAAGTAG ACGTTGGATGAAACCAGTTAACTGAAC 2300427 ACGTTGGATGACAACCCAGTGAAGCAC ACGTTGGATGAAACCAGTTAACTAACTGTAG 226680 ACGTTGGATGAGAGATTACAGGCATGAGCAC ACGTTGGATGAAACTAACTGTGTC 2423131 ACGTTGGATGAGAGATTACAGGCATGAGATATCCTTCCTT	236185	ACGTTGGATGGGGTCACTTGAATTCAGGAG	ACGTTGGATGACTGCAACCACTGCCTCTTG
364652 ACGTTGGATGTTTCTGCTGGGCTGTGATAG ACGTTGGATGGGGAAATGCTCAGCATGTAC 394604 ACGTTGGATGTATTTTGGGATGGTGTGGC ACGTTGGATGGAACCAGGTCTTCCTTGATG 403727 ACGTTGGATGTCACTTGAACCCAGGAGATG ACGTTGGATGGATCCTGCTTTTACCACTTCGC 446658 ACGTTGGATGTCACTGAGTTCAACTCCTTC ACGTTGGATGGTTCCTGCTTTACCACTTCG 451571 ACGTTGGATGTCTCTGGGTGGTTGCTCTCTG ACGTTGGATGAAATAGGCACACTGGAGG 452749 ACGTTGGATGTCCTACTCCAGTATGACCTC ACGTTGGATGGAAGTCCCAACCCCTAATAC 454328 ACGTTGGATGTGCAAACTGGTGCATCAGAG ACGTTGGATGCCTGGTATTTTCATATCGCC 742710 ACGTTGGATGGGCACATGGATATGGTGAAG ACGTTGGATGGCCTCTGTGATGGTGCCC 881118 ACGTTGGATGGGCACATGGATATGGTGAAG ACGTTGGATGAACACACTGGATGCCCC 881118 ACGTTGGATGTATAGCTGAAGCCTGCTTTC ACGTTGGATGACACACCCCAACCCC 910122 ACGTTGGATGTTCTCTTCACTGCTATCT ACGTTGGATGACACACCCCATTCTGAGAAGAG 1005517 ACGTTGGATGTACACTGCTACT ACGTTGGATGAACACCCCAACCTCTGAGAAGAG 1005517 ACGTTGGATGTACACTACTGCTACT ACGTTGGATGAACACCCCCTTGAAAACC 1394095 ACGTTGGATGTCCAACTTCCGC ACGTTGGATGAACACTCCTTGATTGGC 2206817 ACGTTGGATGCAGAAACCCAGTGAAGTAACACCCAACCTCCTTGATTGGC 2206817 ACGTTGGATGCCAGAAACCCAGTGAAGTAACACCACTTGAAAACCACTTGAAGAACCACTTGAAGAACCACTTGAAGAACCACTTGAAGACCACTTCAACTTCACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTAACTAACCACTTAACACACACACACACACACACACACACACACACACACACA	236187	ACGTTGGATGTAGTGAAACTCTGTCTCTGC	ACGTTGGATGACCTGCACCAACCTTTAACC
394604 ACGTTGGATGTATTTTGGGATGGTGTGGGC ACGTTGGATGGAACCAGGTCTTCCTTGATG 403727 ACGTTGGATGTCACTTGAACCCAGGAGATG ACGTTGGATGGATCACAGAGATTTCGC 446658 ACGTTGGATGTCACTGAGTTCAACTCCTTC ACGTTGGATGGATCACTGACTTCGC 451571 ACGTTGGATGTCTCTGGGTGGTTGCTCTCTG ACGTTGGATGAAGTAATGGCACACTGGAGG 452749 ACGTTGGATGTCTACTCCAGTATGACCTC ACGTTGGATGGAAGTAATGGCACACCCCTAATAC 454328 ACGTTGGATGTCCTACTCCAGTATGACCTC ACGTTGGATGGAAGTCCCAACCCCTAATAC 454328 ACGTTGGATGTGCAAACTGGTGCATCAGAG ACGTTGGATGGCCTCGGTATTTTCATATCGCC 742710 ACGTTGGATGGGCACATGGATATGGTGAAG ACGTTGGATGTGCCTCTGTGATGGTGCCC 881118 ACGTTGGATGGACACATGGATATGGTGAAG ACGTTGGATGAAATAGGCACGTGGCTCCCC 881118 ACGTTGGATGTATAGCTGAAGCCTGCTTTC ACGTTGGATGAAAATAGGCACGTGGCTCCCC 910122 ACGTTGGATGGTTCTCTTCACTGCTATCT ACGTTGGATGAACACGCCATTCTGAGAAGAG 1005517 ACGTTGGATGTACTAATGTCAGTGGTAGAA ACGTTGGATGAACACCCCATTCTGAGAAAAC 1394095 ACGTTGGATGTACTAATGTCAGTGGTAGAA ACGTTGGATGAAAACACTCCTTGATTGGC 2206817 ACGTTGGATGACCACACTCCCC ACGTTGGATGAAACCAGTTACTAACTGTAG 2268339 ACGTTGGATGACCAGAAACCCAGTGAAGTAG ACGTTGGATGAAACCAGTTACTAACTGTAG 2268339 ACGTTGGATGATCCTGGAGAGTTATAACCC ACGTTGGATGAAACCAGTTACTAACTGTAG 2300427 ACGTTGGATGATCCTGGAGATTATACCC ACGTTGGATGAAACTAACTGTAG 2326680 ACGTTGGATGAGGCTAATTCCTTCTCCTGG ACGTTGGATGAAACTAACTGTGTC 2423131 ACGTTGGATGATGACCAGAGACTAAGAGTCTGTAG ACGTTGGATGCCAACATCACTGTGTC 2423131 ACGTTGGATGATGCCTGCCTTACGAGAATG ACGTTGGATGCCAACATCACTGTGTC 2876003 ACGTTGGATGGCAAAGACTAAGAGTCTGTAG ACGTTGGATGCCAACATCACTGTGTC 2876003 ACGTTGGATGGCAAAGACTAAGAGTCTGTAG ACGTTGGATGCCAACATCACTGTGTC 2876003 ACGTTGGATGATGCCTGCCTTACGAGAATG ACGTTGGATGCCAACATCACTGTGTC 2876003 ACGTTGGATGATGCCAAGAGCTAAGAGTCTGTAG ACGTTGGATGCCAACATCACTGTGACACTTCTGACAATTCCTTCTCCTAGAAAACCAGAGACTAAGAGTCTGTAGAAACCAGAGTTCTGACAATTCCTTCTCAAGAGATTCCTTCTAGAAAATAGAGCCAAGACTAAGAGTCTGTAGAAACCAGAGACTAAGAGTCTGAAACCAGTTGAGACCAACATCACTGTGTC ACGTTGGATGATGCCAAAGACTAAGAGTCTGTAGAAATATGGACCAACATCACTGTGACAACTCACTGAAAATATGGAACCAATAACTGTGAACAATAAGAGTCTTAAGAAAATAGAGCCAAGACTAAAGAGTCTGAAGAGTCTGTAGACAGAGACTAAGAGTCTGAAACCAATTAAGAGCCAACATCACTGAAAACCAGTTGAAAACCAGTTGAGAAACCAATTAAGAGATTCTGAAAAACA	236189	ACGTTGGATGTGGATTTACAGAAAAACTGC	ACGTTGGATGCTGTGAGACACTAGGGATAC
403727 ACGTTGGATGTCACTTGAACCCAGGAGATG ACGTTGGATGGTTTTGAGACAGAGTTTCGC 446658 ACGTTGGATGTCACTGAGTTCAACTCCTTC ACGTTGGATGGTTCCTGCTTTACCACTTCG 451571 ACGTTGGATGTCCTGCGTGGTGCTCTCTG ACGTTGGATGATAATGGCACACTGGAGG 452749 ACGTTGGATGTCCTACTCCAGTATGACCTC ACGTTGGATGAAGTCACCAACCCCTAATAC 454328 ACGTTGGATGTGCAAACTGGTGCATCAGAG ACGTTGGATGCCTCGTGTATTTTCATATCGCC 742710 ACGTTGGATGGGCACATGGATATGGTGAAG ACGTTGGATGGCCTCTGTGATGGTGCCC 742711 ACGTTGGATGGGCACATGGATATGGTGAAG ACGTTGGATGAAATAGGCACGTGGCTCCCC 881118 ACGTTGGATGGTCAAGCCTGCTTTC ACGTTGGATGACACGCCATTCTGAGAGAGAACACC 910122 ACGTTGGATGGTTTCTCTCACTGCTATCT ACGTTGGATGACACGCCATTCTGAGAAGAGA 1005517 ACGTTGGATGTCAATGTCAGTGGTAGAG ACGTTGGATGAACACCCCATTCTGAGAAGAG 1005517 ACGTTGGATGTCAATGTCAGTGGTAGAG ACGTTGGATGCAAACCTGGCTGAAAAC 1394095 ACGTTGGATGTCAGTGATCCAACTTCCGC ACGTTGGATGACACCACTTGCTGATTGGC 2206817 ACGTTGGATGGCAGAAACCCAGTGAAGTAG ACGTTGGATGAAAACCAGTTACTAACTGTAG 2268339 ACGTTGGATGACCAGAAACCCAGTGAAGTAA ACGTTGGATGAAAACCAGTTACTAACTGTAG 2268339 ACGTTGGATGACACCAGTGAAGTAG ACGTTGGATGAAAACCAGTTAACTGTAG 2268339 ACGTTGGATGACACACTCCGCAACTCCTGGAAGACCACTGTACTAACTGTAG 2268339 ACGTTGGATGACACACTCCGGAGATGTAACACCAACTCCTTCTGACACC 2300427 ACGTTGGATGACACACTCCGGAGATGTAACACCACCACCACCTGCTTCCTGCACACCACCACCACCACCACCACCACCACCACCACCACC	364652	ACGTTGGATGTTTCTGCTGGGCTGTGATAG	ACGTTGGATGGGGAAATGCTCAGCATGTAC
446658 ACGTTGGATGTCACTGAGTTCACTCCTTC ACGTTGGATGGTTCCTGCTTTACCACTTCG 451571 ACGTTGGATGTTCTGGGTGGTTGCTCTCTG ACGTTGGATGAGTAATGGCACACTGGAGG 452749 ACGTTGGATGTCCTACTCCAGTATGACCTC ACGTTGGATGGAAGTCCCAACCCCTAATAC 454328 ACGTTGGATGTCCAAACTGGTGCATCAGAG ACGTTGGATGCCTGGTATTTTCATATCGCC 742710 ACGTTGGATGGCCACACTGGATATGGTGAAG ACGTTGGATGTGCCTCTGTGATGGTGCCC 742711 ACGTTGGATGGGCACATGGATATGGTGAAG ACGTTGGATGAAATAGGCACGTGGCTCCCC 881118 ACGTTGGATGATATAGCTGAAGCCTGCTTTC ACGTTGGATGAAGAAACACCC 910122 ACGTTGGATGGTTTCTCTTCACTGCTATCT ACGTTGGATGACACGCCATTCTGAGAAGAGA 1005517 ACGTTGGATGATCACATGTCAGTGGTAGAG ACGTTGGATGAAGACACCTGGCTGAAAAC 1394095 ACGTTGGATGTCAGTGATCCAACTTCCGC ACGTTGGATGAAACCCAGTTACTAACTGTAG 2268339 ACGTTGGATGGCAGAAACCCAGTGAAGTAG ACGTTGGATGAAACCCAGTTACTAACTGTAG 2268339 ACGTTGGATGACACACCAGTGAAGTAG ACGTTGGATGAAACCCAGTTACTAACTGTAG 2300427 ACGTTGGATGAGAATCCTGGAGATGTTATACCC ACGTTGGATGAAGCTCAAC 2300427 ACGTTGGATGAGATTACAGGCATGAGCCAC ACGTTGGATGAAGTTAAATAAGCTCTTCTG 2326680 ACGTTGGATGAGGCTAATTCCTTCCTGG ACGTTGGATGAAGTTAAATAAGCTCTTCTG 2326680 ACGTTGGATGAGGCTAATTCCTTCCTGG ACGTTGGATGAACATCACTGTGTC 2423131 ACGTTGGATGATGAAGCCTAACAGAATATGTGAAC 2876003 ACGTTGGATGATGCAAAGACCTAAGAGTCTGTAG ACGTTGGATGCCAGATTCTGACATT	394604	ACGTTGGATGTATTTTGGGATGGTGTGGGC	ACGTTGGATGGAACCAGGTCTTCCTTGATG
451571 ACGTTGGATGTTCTGGGTGGTTGCTCTCTG ACGTTGGATGAAGTAATGGCACACTGGAGG 452749 ACGTTGGATGTCCTACTCCAGTATGACCTC ACGTTGGATGAAGTCCCAACCCCTAATAC 454328 ACGTTGGATGTGCAAACTGGTGCATCAGAG ACGTTGGATGCCTGGTATTTTCATATCGCC 742710 ACGTTGGATGGGCACATGGATATGGTGAAG ACGTTGGATGTGCCTCTGTGATGGTGCCC 742711 ACGTTGGATGGGCACATGGATATGGTGAAG ACGTTGGATGAAAATAGGCACGTGGCTCCCC 881118 ACGTTGGATGGTATAGCTGAAGCCTGCTTTC ACGTTGGATGAAGAAGAGAAACACC 910122 ACGTTGGATGGTTTCTCTTCACTGCTATCT ACGTTGGATGACACGCCATTCTGAGAAGAG 1005517 ACGTTGGATGTACTAATGTCAGTGGTAGAG ACGTTGGATGAAGACACCCCCTTGAAAACC 1394095 ACGTTGGATGTTCAGTGATCCAACTTCCGC ACGTTGGATGAAACCCCCTTGATTGGC 2206817 ACGTTGGATGGCAGAAACCCAGTGAAGTAG ACGTTGGATGAAACCCAGTTACTAACTGTAG 2268339 ACGTTGGATGATCCTGGAGAATGTATACCC ACGTTGGATGAAACCAGCTGGTTAACACTGTAG 2300427 ACGTTGGATGACGAGATGTTATACCC ACGTTGGATGAAGATTAAAACCTCTTCTG 2326680 ACGTTGGATGAGGCTAATTCCTTCTCCTGG ACGTTGGATGAAGATTAAAACACTCTTCTG 2423131 ACGTTGGATGAGGCAAAGACTAAGAGTCTTACAACACACCCCCCCC	403727	ACGTTGGATGTCACTTGAACCCAGGAGATG	ACGTTGGATGGTTTTGAGACAGAGTTTCGC
452749 ACGTTGGATGTCCTACTCCAGTATGACCTC ACGTTGGATGGAAGTCCCAACCCCTAATAC 454328 ACGTTGGATGTGCAAACTGGTGCATCAGAG ACGTTGGATGCCTGGTATTTTCATATCGCC 742710 ACGTTGGATGGGCACATGGATATGGTGAAG ACGTTGGATGTGCCTCTGTGATGGTGTCCC 742711 ACGTTGGATGGGCACATGGATATGGTGAAG ACGTTGGATGAAATAGGCACGTGGCTCCCC 881118 ACGTTGGATGTATAGCTGAAGCCTGCTTTC ACGTTGGATGACACGCAGTGAAGACACCC 910122 ACGTTGGATGGTTCTCTTCACTGCTATCT ACGTTGGATGACACGCCATTCTGAGAAGAG 1005517 ACGTTGGATGTACTAATGTCAGTGGTAGAG ACGTTGGATGAACACCCCCTTCTGAGAAACC 1394095 ACGTTGGATGTCAGTGATCCAACTTCCGC ACGTTGGATGCCAAACTCCTTGATTGGC 2206817 ACGTTGGATGGCAGAAACCCAGTGAAGTAG ACGTTGGATGAAACCCAGTTACTAACTGTAG 2268339 ACGTTGGATGACCCAGTGAAGTAG ACGTTGGATGAAACCCAGTTACTAACTGTAG 2300427 ACGTTGGATGACACTCCTGGAGATGTTATACCC ACGTTGGATGAAGCTTAAATAAGCTCTTCTG 2326680 ACGTTGGATGAGAGTTACAGGCATGAGCCAC ACGTTGGATGAAACTCACTGTGTC 2423131 ACGTTGGATGAGGCTAATTCCTTCTCCTGG ACGTTGGATGTCACTAGAATATGTGAAC 2876003 ACGTTGGATGATGCCTGCCTTACGAGAATG ACGTTGGATGTCACTAGAATATGTGAAC ACGTTGGATGGATGATGCCTGCCTTACGAGAATG ACGTTGGATGTCACTAGAATATGTGAAC	446658	ACGTTGGATGTCACTGAGTTCAACTCCTTC	ACGTTGGATGGTTCCTGCTTTACCACTTCG
454328 ACGTTGGATGTGCAAACTGGTGCATCAGAG ACGTTGGATGCCTGGTATTTTCATATCGCC 742710 ACGTTGGATGGGCACATGGATATGGTGAAG ACGTTGGATGTGCCTCTGTGATGGTGTCCC 742711 ACGTTGGATGGGCACATGGATATGGTGAAG ACGTTGGATGAAAAAAAAAA	451571	ACGTTGGATGTTCTGGGTGGTTGCTCTCTG	ACGTTGGATGAAGTAATGGCACACTGGAGG
742710 ACGTTGGATGGCACATGGATATGGTGAAG ACGTTGGATGTGCCTCTGTGATGGTGCCC 742711 ACGTTGGATGGGCACATGGATATGGTGAAG ACGTTGGATGAAATAGGCACGTGGCTCCCC 881118 ACGTTGGATGTATAGCTGAAGCCTGCTTTC ACGTTGGATGACACGCCATTCTGAGAAGACACCC 910122 ACGTTGGATGGTTTCTCTTCACTGCTATCT ACGTTGGATGACACGCCATTCTGAGAAGAG 1005517 ACGTTGGATGTACTAATGTCAGTGGTAGAG ACGTTGGATGTGAAGACACTGGCTGAAAAC 1394095 ACGTTGGATGTTCAGTGATCCAACTTCCGC ACGTTGGATGCCAAACTCCTTGATTGGC 2206817 ACGTTGGATGGCAGAAACCCAGTGAAGTAG ACGTTGGATGAAACCAGTTACTAACTGTAG 2268339 ACGTTGGATGATCCTGGAGATGTTATACCC ACGTTGGATGCCTGGTGTTTAAGGCTCAAC 2300427 ACGTTGGATGAGATTACAGGCATGAGCCAC ACGTTGGATGAAGTTAAATAAGCTCTTCTG 2326680 ACGTTGGATGAGGCTAATTCCTTCTCCTGG ACGTTGGATGTCAACATCACTGTGTC 2423131 ACGTTGGATGAGGCTAATTCCTTCTCCTGG ACGTTGGATGTCACCTAGAATATGTGAAC 2876003 ACGTTGGATGGCAAAGACTAAGAGTCTGTAG ACGTTGGATGCTGAGCCAGATTCTGACATT	452749	ACGTTGGATGTCCTACTCCAGTATGACCTC	ACGTTGGATGGAAGTCCCAACCCCTAATAC
742711 ACGTTGGATGGCACATGGATATGGTGAAG ACGTTGGATGAAATAGGCACGTGGCTCCCC 881118 ACGTTGGATGTATAGCTGAAGCCTGCTTTC ACGTTGGATGTAGCAGTGAAGAAACACC 910122 ACGTTGGATGGTTCTCTTCACTGCTATCT ACGTTGGATGACACGCCATTCTGAGAAGAG 1005517 ACGTTGGATGTACTAATGTCAGTGGTAGAG ACGTTGGATGTGAAGACACCTGGCTGAAAAC 1394095 ACGTTGGATGTTCAGTGATCCAACTTCCGC ACGTTGGATGCCAAACTCCTTGATTGGC 2206817 ACGTTGGATGGCAGAAACCCAGTGAAGTAG ACGTTGGATGAAACCAGTTACTAACTGTAG 2268339 ACGTTGGATGATCCTGGAGATGTTATACCC ACGTTGGATGCCTGGTGTTTAAGGCTCAAC 2300427 ACGTTGGATGAGATTACAGGCATGAGCCAC ACGTTGGATGAAGTTAAATAAGCTCTTCTG 2326680 ACGTTGGATGAGGCTAATTCCTTCTCCTGG ACGTTGGATGTCACAACATCACTGTGTC 2423131 ACGTTGGATGATGCCTGCCTTACGAGAATG ACGTTGGATGTCACCTAGAATATGTGAAC ACGTTGGATGGATGGCAAAGACTAAGAGTCTGTAG ACGTTGGATGCTGAGCCAGATTCTGACATT	454328	ACGTTGGATGTGCAAACTGGTGCATCAGAG	ACGTTGGATGCCTGGTATTTTCATATCGCC
881118 ACGTTGGATGTATAGCTGAAGCCTGCTTTC ACGTTGGATGTAGCAGTGAAGAGAAACACC 910122 ACGTTGGATGGTTCTCTCTCACTGCTATCT ACGTTGGATGACACGCCATTCTGAGAAGAG 1005517 ACGTTGGATGTACTAATGTCAGTGGTAGAG ACGTTGGATGTGAAGACACTGGCTGAAAAC 1394095 ACGTTGGATGTCAGTGATCCAACTTCCGC ACGTTGGATGCCAAACTCCTTGATTGGC 2206817 ACGTTGGATGGCAGAAACCCAGTGAAGTAG ACGTTGGATGAAACCAGTTACTAACTGTAG 2268339 ACGTTGGATGATCCTGGAGATGTTATACCC ACGTTGGATGACCTGGTGTTTAAGGCTCAAC 2300427 ACGTTGGATGAGATTACAGGCATGAGCCAC ACGTTGGATGAAGTTAAATAAGCTCTTCTG 2326680 ACGTTGGATGAGGCTAATTCCTTCTCCTGG ACGTTGGATGTCGTACAACATCACTGTGTC 2423131 ACGTTGGATGATGCCTGCCTTACGAGAATG ACGTTGGATGTCACTAGAATATGTGAAC 2876003 ACGTTGGATGGCAAAGACTAAGAGTCTGTAG ACGTTGGATGCTGAGCCAGATTCTGACATT	742710	ACGTTGGATGGGCACATGGATATGGTGAAG	ACGTTGGATGTGCCTCTGTGATGGTGTCCC
910122 ACGTTGGATGGTTTCTCTCACTGCTATCT ACGTTGGATGACACGCCATTCTGAGAAGAG 1005517 ACGTTGGATGTACTAATGTCAGTGGTAGAG ACGTTGGATGTGAAGACACTGGCTGAAAAC 1394095 ACGTTGGATGTTCAGTGATCCAACTTCCGC ACGTTGGATGCCAAACTCCTTGATTGGC 2206817 ACGTTGGATGGCAGAAACCCAGTGAAGTAG ACGTTGGATGAAACCAGTTACTAACTGTAG 2268339 ACGTTGGATGATCCTGGAGATGTTATACCC ACGTTGGATGACCTGGTGTTTAAGGCTCAAC 2300427 ACGTTGGATGAGATTACAGGCATGAGCCAC ACGTTGGATGAAGTTAAATAAGCTCTTCTG 2326680 ACGTTGGATGAGGCTAATTCCTTCTCCTGG ACGTTGGATGTCGCAACATCACTGTGTC 2423131 ACGTTGGATGATGCCTGCCTTACGAGAATG ACGTTGGATGTCACTAGAATATGTGAAC 2876003 ACGTTGGATGGCAAAGACTAAGAGTCTGTAG ACGTTGGATGCTGAGCCAGATTCTGACATT	742711	ACGTTGGATGGGCACATGGATATGGTGAAG	ACGTTGGATGAAATAGGCACGTGGCTCCCC
1005517 ACGTTGGATGTACTAATGTCAGTGGTAGAG ACGTTGGATGTAAAGCACTGGCTGAAAAC 1394095 ACGTTGGATGTTCAGTGATCCAACTTCCGC ACGTTGGATGCCAAACTCCTTGATTGGC 2206817 ACGTTGGATGGCAGAAACCCAGTGAAGTAG ACGTTGGATGAAACCAGTTACTAACTGTAG 2268339 ACGTTGGATGATCCTGGAGATGTTATACCC ACGTTGGATGCCTGGTGTTTAAGGCTCAAC 2300427 ACGTTGGATGAGATTACAGGCATGAGCCAC ACGTTGGATGAAGTTAAATAAGCTCTTCTG 2326680 ACGTTGGATGAGGCTAATTCCTTCTCCTGG ACGTTGGATGTCCAACATCACTGTGTC 2423131 ACGTTGGATGATGCCTGCCTTACGAGAATG ACGTTGGATGTCACTAGAATATGTGAAC 2876003 ACGTTGGATGGCAAAGACTAAGAGTCTGTAG ACGTTGGATGCTGAGCCAGATTCTGACATT	881118	ACGTTGGATGTATAGCTGAAGCCTGCTTTC	ACGTTGGATGTAGCAGTGAAGAGAAACACC
1394095 ACGTTGGATGTCAGTGATCCAACTTCCGC ACGTTGGATGCCAAACTCCTTGATTGGC 2206817 ACGTTGGATGGCAGAAACCCAGTGAAGTAG ACGTTGGATGAAACCAGTTACTAACTGTAG 2268339 ACGTTGGATGATCCTGGAGATGTTATACCC ACGTTGGATGACCTGGTGTTTAAGGCTCAAC 2300427 ACGTTGGATGAGATTACAGGCATGAGCCAC ACGTTGGATGAAGTTAAATAAGCTCTTCTG 2326680 ACGTTGGATGAGGCTAATTCCTTCTCCTGG ACGTTGGATGTCGCAACATCACTGTGTC 2423131 ACGTTGGATGATGCCTGCCTTACGAGAATG ACGTTGGATGTCACTAGAATATGTGAAC 2876003 ACGTTGGATGGCAAAGACTAAGAGTCTGTAG ACGTTGGATGCTGAGCCAGATTCTGACATT	910122	ACGTTGGATGGTTTCTCTTCACTGCTATCT	ACGTTGGATGACACGCCATTCTGAGAAGAG
2206817 ACGTTGGATGGCAGAAACCCAGTGAAGTAG ACGTTGGATGAAACCAGTTACTAACTGTAG 2268339 ACGTTGGATGATCCTGGAGATGTTATACCC ACGTTGGATGCCTGGTGTTTAAGGCTCAAC 2300427 ACGTTGGATGAGATTACAGGCATGAGCCAC ACGTTGGATGAAGTTAAATAAGCTCTTCTG 2326680 ACGTTGGATGAGGCTAATTCCTTCTCCTGG ACGTTGGATGTCCAACATCACTGTGTC 2423131 ACGTTGGATGATGCCTGCCTTACGAGAATG ACGTTGGATGTCACTAGAATATGTGAAC 2876003 ACGTTGGATGGCAAAGACTAAGAGTCTGTAG ACGTTGGATGCTGAGCCAGATTCTGACATT	1005517	ACGTTGGATGTACTAATGTCAGTGGTAGAG	ACGTTGGATGTGAAGACACTGGCTGAAAAC
2268339 ACGTTGGATGATCCTGGAGATGTTATACCC ACGTTGGATGCCTGGTGTTTAAGGCTCAAC 2300427 ACGTTGGATGAGATTACAGGCATGAGCCAC ACGTTGGATGAAGTTAAATAAGCTCTTCTG 2326680 ACGTTGGATGAGGCTAATTCCTTCTCCTGG ACGTTGGATGTCCAACATCACTGTGTC 2423131 ACGTTGGATGATGCCTGCCTTACGAGAATG ACGTTGGATGTCACTAGAATATGTGAAC 2876003 ACGTTGGATGGCAAAGACTAAGAGTCTGTAG ACGTTGGATGCTGAGCCAGATTCTGACATT	1394095	ACGTTGGATGTTCAGTGATCCAACTTCCGC	ACGTTGGATGCCAAACTCCTTGATTGGC
2300427 ACGTTGGATGAGATTACAGGCATGAGCCAC ACGTTGGATGAAGTTAAATAAGCTCTTCTG 2326680 ACGTTGGATGAGGCTAATTCCTTCTCCTGG ACGTTGGATGTCCAACATCACTGTGTC 2423131 ACGTTGGATGATGCCTGCCTTACGAGAATG ACGTTGGATGTCACTAGAATATGTGAAC 2876003 ACGTTGGATGGCAAAGACTAAGAGTCTGTAG ACGTTGGATGCTGAGCCAGATTCTGACATT	2206817	ACGTTGGATGGCAGAAACCCAGTGAAGTAG	ACGTTGGATGAAACCAGTTACTAACTGTAG
2326680 ACGTTGGATGAGGCTAATTCCTTCTCTGG ACGTTGGATGTCGTAACATCACTGTGTC 2423131 ACGTTGGATGATGCCTGCCTTACGAGAATG ACGTTGGATGTCACTAGAATATGTGAAC 2876003 ACGTTGGATGGCAAAGACTAAGAGTCTGTAG ACGTTGGATGCTGAGCCAGATTCTGACATT	2268339	ACGTTGGATGATCCTGGAGATGTTATACCC	ACGTTGGATGCCTGGTGTTTAAGGCTCAAC
2423131 ACGTTGGATGATGCCTGCCTTACGAGAATG ACGTTGGATGTCACTAGAATATGTGAAC 2876003 ACGTTGGATGGCAAAGACTAAGAGTCTGTAG ACGTTGGATGCTGAGCCAGATTCTGACATT	2300427	ACGTTGGATGAGATTACAGGCATGAGCCAC	ACGTTGGATGAAGTTAAATAAGCTCTTCTG
2876003 ACGTTGGATGGCAAAGACTAAGAGTCTGTAG ACGTTGGATGCTGAGCCAGATTCTGACATT	2326680	ACGTTGGATGAGGCTAATTCCTTCTCCTGG	ACGTTGGATGTCGTGCAACATCACTGTGTC
	2423131	ACGTTGGATGATGCCTGCCTTACGAGAATG	ACGTTGGATGTGTCACTAGAATATGTGAAC
3761873 ACGTTGGATGCTGTCCCTCTTAGAGCAATG ACGTTGGATGCTATGAGCCTTTGACACAGC	2876003	ACGTTGGATGGCAAAGACTAAGAGTCTGTAG	ACGTTGGATGCTGAGCCAGATTCTGACATT
	3761873	ACGTTGGATGCTGTCCCTCTTAGAGCAATG	ACGTTGGATGCTATGAGCCTTTGACACAGC

TABLE 20

dbSNP rs#	Extend Primer (SEQ ID NOS 1077-1179)	Term Mix
54144	CTGAAAGACACCATTTAT	CGT
183535	GTCCTGCACAAGACTTTGATA	ACG
236104	CCCATTTCATACCACCTATCA	ACG
236105	CTCCCTCCTCGTGAGACC	ACT
236113	GATCATTCATGAAACAGATTCTA	ACG
236119	TGTTCTCAAGGAAAAAGAAAAA	ACT
236120	GATCATCCCTGGGAATGGTA	ACT
236122	GAGGCAGGGAATCAGCAATA	ACT
236143	ACCCCAAATAGGTAAAGATCTGT	ACT
236145	CTCCTGCACTGAGCTCCTAT	ACT
236146	TATCTCCGCCCTAAGAATACT	ACT
236149	GAAATATTAGAATTTAGAGGCAG	ACT
236160	GAGTTTTTATGAGAAAGGGCAA	ACT
236162	GTTGTTTTAAAGTGTTGGTTGTAA	ACT
236163	CAATACATAGTGAAGCTTTGGG	ACT
236164	CTGGTGTCACACACACATGTA	ACT ·
236166	GGAACATCTCAGAAAAAAA	CGT

236167	CTTGTGCAGGACTTAGACCA	ACT
236176	ATAGGCTTTCTTGTGTATTTGCA	ACT
236177	AGTGAGGGGAAGCAGAGTC	CGT
236180	ACTTGGGAATTAGGTGGAGG	ACG
236182	GTTCAGAGATAATGCTGCTGATC	CGT
236183	GAAATCCCACAGGAACACAAT	ACT
236184	CCCAGCAAATAACAAGAATTGGCC	ACT
379418	CTTAAGCCAAGACAAACA	ACG
400735	TTCATCTTCCACCCTGGCC	ACT_
409035	TGCTTTGCTTGCCTCCCACA	ACG
440005	GCTGTCCTTTTTACAAGGAAAT	ACT
446614	TAAAGACTGAAGCTTTCACAGT	ACT
451417	CGTTATCACCATTGGGCTTTA	CGT
454422	GATCCTTCTCACTTACTGTTC	ACT
500277	GATTATGCCCTGAGGTCTTTTG	ACT
540717	AACCCAACAAATCCTAGGGC	ACG
546106	GATGGGCTCCCCATATGAC	ACT
571039	TGTAGCAGGCAACTGAGCAGGAGA	CGT
1039542	GAACACCCTCCAGCACAAG	ACT
1039543	AGAAGAGCTTTCATCTGTGTG	ACT
1343180	CACAGCCCTCCATTACAGC	ACT
CHGB SNP2	GTATGTTTGTGTTCCATTTGCA	ACT
rs384578	GTATGTTTGTGTTCCATTTGCA	ACT
rs742710	GAAGAGAGGGCCTTGAGC	ACG
rs742711	TCCCCTGCCTCTGTGATGG	ACG
rs881118	CTGAAGCCTGCTTTCTTTCAT	ACT
rs910122	CTTCACTGCTATCTTCCCCT	ACG
CHGB SNP1	TCTTGGAGCCCTGTATTC	ACG
180477	GTGGCTCACGCCTATAA	CGT
236102	GTTCTCTCTGAAACCTGTTA	ACT
236103	CATGCACCAGCTGTGTG	ACT
236106	GAACATTCCAGGCAAAC	ACT
236107	GTTCTGGTAAAAAAAAAGTTTG	CGT
236108	CTGTTGAACCCAGAAATATC	ACT
236109	CACTAGCCACCACGCCC	ACT
236110	CAATGTTGACTGCATTGACT	ACT
236111	GTTCTGAGGTTACCAGA	ACT
236112	ACCATCCTAGCTAACACG	ACT
236114	AATCACAAGTACCTCGAATAC	ACT
236115	AGGTAAGTGGCAGAACT	ACT
236116	TCAGGCAAGCACAGTACAAA	ACG
236117	GCCTCCCAAGTAGCTGG	ACT
236118	CCCTAATCTGAAAATCTGAAATCT	ACT
236121	AAGAATTTTCTTATTCAACTGTC	ACT
236121 236123	AAGAATTTTCTTATTCAACTGTC CTTCACTAAATAAAAATGTGTCC	ACT

236125	TTTAACTCCTAGCTTTTAAAGA	ACG
236148	AATGTGGCTGGTCCGATCTG	ACT
236151	ATTCTCCTGGCTCCCTG	ACG
236152	TTATCCAGGCGTCCAGG	ACT
236154	TGATGCCACTGGTCAGG	ACT
236155	AATTCCCCTTTGCACTCAT	ACT
236158	TTACAACTGTAAGCCACCGC	ACT
236159	CCTGACCTCGTGATCTG	ACG
236161	CTCTAGGCTAGTATTAATTTTTGT	ACT
236165	TAACGCCTGTAATCCCA	ACT
236168	ACTTGCATGTGTATGTATATCT	ACT
236169	ATGTCTTTTCCCCCTCT	ACT
236171	AAGTGCTGGGATTACAGATA	ACG
236173	TTGCTCCCTCTCCCCTT	ACT
236175	CACTGCATCAAGATGGGCC	ACG
236179	CAGGTTTGACTCAAAACTTTAA	ACG
236181	ATGTCTTTTCTGTACTGGATA	ACT
236185	TACTGAGGAGGCTGAGG	ACG
236187	AACTCTGTCTCTGCAAAAAA	ACT
236189	CAGAAAAACTGCACAAAAA	ACT
364652	CTGTGATAGGAAAAAGGAA	ACT
394604	CCAGCAGAGGCAAAAATAAGA	ACG
403727	TGCCACTGCACTCCAGCCT	ACT
446658	AGGAAAAGAGAGGCAAAC	ACT
451571	GCTGTCTTCATTCTCTTGT	ACG
452749	CCTATTTTCAAGTCAGGT	ACG
454328	CCTAAACAGCAGTTTTAGTACAT	ACG
742710	AGAGAGGGCCTTGAGC	ACG
742711	TGAGCCGGGAAAGGGAC	ACT
881118	TGAAGCCTGCTTTCTTTCAT	ACT_
910122	CTTCACTGCTATCTTCCCCT	ACG
1005517	GGTAGAGAATGTAATAACAGT	ACT
1394095	ACGAGAGGGGCGGGCG	ACT
2206817	TTAGAGCAGGGCAGGGG	ACT
2268339	CAGAATGCTGAGATGGC	ACT
2300427	CACCCGGCCGGGAAAAT	ACT
2326680	TGGAATTTGAGAAGGCCTG	ACT
2423131	GCCTTACGAGAATGTTATTT	CGT
2876003	AGAGTCTGTAGTCCCAA	ACT
3761873	TGTATTTCCATAGTAATTTGCTC	ACT

Please delete paragraph [0274] and replace it with the following paragraph:

[0274] The methods used to verify and genotype the proximal SNP of Table 21 are the same methods described in Examples 1 and 2 herein. The PCR primers and extend primers used in these assays are provided in Table 22 and Table 23, respectively.

TABLE 22

dbSNP rs#	First PCR primer (SEQ ID NOS 619-620)	Second PCR primer (SEQ ID NOS 621-622)
742710	ACGTTGGATGGACATGAAATAGGCACGTGG	ACGTTGGATGAGAAAGTGAGGAAGAGAGGG
236110	ACGTTGGATGTCACTCTGTTTCTACTAACC	ACGTTGGATGATCGATCCAATGTTGACTGC

TABLE 23

dbSNP rs#	Extend Primer <u>(SEQ ID NOS 623-624)</u>	Term Mix
742710	AGAGAGGGCCTTGAGC	ACG
236110	AATGTTGACTGCATTGACT	ACT

Please delete paragraph [0277] and replace it with the following paragraph:

[0277] The methods used to verify and allelotype the proximal SNPs of Table 25 are the same methods described in Examples 1 and 2 herein. The PCR primers and extend primers used in these assays are provided in Table 26 and Table 27, respectively.

TABLE 26

dbSNP rs#	Forward PCR primer <u>(SEQ ID NOS 625-660)</u>	Reverse PCR primer (SEQ ID NOS 661-696)
752373	ACGTTGGATGTATCACAAGAACAGCATGGG	ACGTTGGATGATGGTTTCTGTAATCCCCCC
763470	ACGTTGGATGAAGAGGAGTGGCTGATAATG	ACGTTGGATGAAGCAGAAAACTTTGTGCCG
763471	ACGTTGGATGGCAGGTCATGGATTTATTG	ACGTTGGATGCATCATTCCTCTGTGAGGCG
763471	ACGTTGGATGGTGAAGAGCTCTGAAATGCC	ACGTTGGATGTAACTCCTGTGTGGCTTTCT
899011	ACGTTGGATGAAGGTGGAGCCTGCCTCAAG	ACGTTGGATGAGCTTTGCACCCTGTGATGC
899011	ACGTTGGATGAAGGTGGAGCCTGCCTCAAG	ACGTTGGATGAGCTTTGCACCCTGTGATGC
922359	ACGTTGGATGTCAAGCGATCCTCTTCAGCC	ACGTTGGATGATTCATTCCAAGACCGGGTG

930672	ACGTTGGATGGTGGGTTACTTGGTCCATAC	ACGTTGGATGACAGAGCAAGACCTTCTCTC
936513	ACGTTGGATGGTATGAAGTTCTTTGCAGAGT	ACGTTGGATGTACTACTGCACTCCAGCCTG
1375999	ACGTTGGATGCCATTCTTTTACCTTGAACC	ACGTTGGATGCAGAGACTTGCAGAATGGAC
1376000	ACGTTGGATGATAGCTGATGGTGTGCTGAG	ACGTTGGATGAAGCTTGCCTCCCAAGTTAG
1376001	ACGTTGGATGCAAACAATCCCATTACACAG	ACGTTGGATGCAGTACAACAGGGTGGCTATC
1450270	ACGTTGGATGCCATATCACATGGATATGAGG	ACGTTGGATGCATGGCTTCTCTTACACCTG
1450273	ACGTTGGATGGCTGCATATAAGAGACACATG	ACGTTGGATGGCCACTCCAGCTTTCTTTTG
1450274	ACGTTGGATGTGAGAGGAAGCCTGGTGTTG	ACGTTGGATGAAGCTTGCCTCCCAAGTTAG
1562781	ACGTTGGATGTATGTCTCCTGCCTTCTTCC	ACGTTGGATGGGAAAGAAGCTTGATGTGGC
2071019	ACGTTGGATGGGTAAACAACTGACCCATCC	ACGTTGGATGCCTGGGAAATAACCATGAGC
2071020	ACGTTGGATGAATTCACAGCTAAGCCTCCC	ACGTTGGATGTTCAGCTCCAGCTGCATGTT
2198008	ACGTTGGATGGTAGAAGTTTAGTATATGATG	ACGTTGGATGCCCTGTCATTTCAAATACCG
2198009	ACGTTGGATGCTTGTGCCAATCCCACAATG	ACGTTGGATGGCAGAAGTCTAGCCAAGAAC
2198010	ACGTTGGATGCTTGTGCCAATCCCACAATG	ACGTTGGATGAATGCAGAAGTCTAGCCAAG
2403330	ACGTTGGATGTAACTCTGAGACCCAAGGAC	ACGTTGGATGCCAGACAGTTGTGTGTTGAC
2923115	ACGTTGGATGGGATTACCCTAAGGATCCAC	ACGTTGGATGAGAGGAATTCAGTTGCTGCC
2923117	ACGTTGGATGTTGAGTCCAAGAGGTTGAGG	ACGTTGGATGAGACAGTCTTGCTCTGTCAC
2957666	ACGTTGGATGTACTTGGGAGACTGAGGTAG	ACGTTGGATGGCATAGTGGTGTGATCATGG
2957667	ACGTTGGATGAGAATGGTCTTTCCCACTCC	ACGTTGGATGATGGATTACGGAAGGAATAC
2957669	ACGTTGGATGTACTGAGACTCCCAGCATTG	ACGTTGGATGGTGTGCAGCTTAGTAAGTGC
2957670	ACGTTGGATGTCATGTGATTCTCCTGCCTC	ACGTTGGATGGTGAAACCCCGTCTCTACTA
2957675	ACGTTGGATGAGAATGACTTGGGTTTTGGG	ACGTTGGATGCAGTGAGTTGTGACAGCACC
2957677	ACGTTGGATGGTCTTTCTCAATCCCAGCAC	ACGTTGGATGACGAGATCTCCTTGTGTTGC
2957678	ACGTTGGATGAAGACCTCAGGATGTGATGC	ACGTTGGATGATGACCCCGTTTCTTTGCAC
2957679	ACGTTGGATGAGTTCGTCAGAGAGATGTCC	ACGTTGGATGGAGCACATGGATTCACAGAG
3741043	ACGTTGGATGGACATCAGAAGCTAATTGGG	ACGTTGGATGCTTCTTAATGGTAGGGCCAG
3741044	ACGTTGGATGTTTGTTATGCAGAGGTGGCC	ACGTTGGATGTAGATGGGCTCTTCTTGGAC
3741045	ACGTTGGATGAACTGAGCTTCAGACTTCCC	ACGTTGGATGTCAGACCTGTAGATGGGCTC
3891547	ACGTTGGATGGCCATCAAGTTTGTGGCAAT	ACGTTGGATGAAGCTATATGGAGCCCAAGG

TABLE 27

dbSNP rs#	Extend Primer <u>(SEQ ID NOS 697-732)</u>	Term Mix
752373	GGGACCAGGTGGAGATAA	ACG
763470	AGAAAACTTTGTGCCGTTTTCT	ACT
763471	CCAGGCAGCAACTCCCT	ACT
763471	CTCCAAGCAGTAAAGATGTTC	CGT
899011	TTGGTTTTAGAGGATTGCTCC	ACG'
899011	GGTTTTAGAGGATTGCTCC	ACG
922359	TCATGCCTATAATCCAAGCA	ACT
930672	AAAAGCAAGAAACAACAGCA	CGT
936513	AGACAGGGTGAGACCTC	ACT
1375999	TATGCTGCATATAAGAGACACAT	ACT
1376000	ACATATTTCTGGTCTCCA	ACT

ACAGGGTGGCTATCATTAAC	ACT
TGTGAACTGAAAAGTCAAG	ACT
CTTGAACCTATTTCTGTTTTT	ACT
CTCCCAAGTTAGATTGGTTA	ACT
CTTGATGTGGCTGAAGT	CGT
GTGCTGTTGAAATCCTGGG	ACT
AACCCTTTGTCAGCTGAA	ACT
CAGGCTTTTGGCTAAGATCAAG	ACT
AGTGAAGAATTTTCCCTATTAGAT	ACT
AAGTCTAGCCAAGAACATTT	ACT
CTCCCACTCCTCTCATCAG	ACT
GTTGCTGCCCGCTTTCC	ACG
CTCTGTCACCCATGCTGGA	ACT
ACCTCCTGGGCTCAAGC	ACT
GGAAGGAATACTAAAGAACAA	CGT
AGTAAGTGCTGTGATGCACC	ACT
TAGCTGAGCATGGTGGC	ACT
AGCATGGGTGACAGAGC	ACT
TGTGTTGCCCAGACTAG	ACT
ACTCCCTGGCCTCCCCT	ACG
TCACAGAGCTGCCAGGG	ACT
CAAAATTCTCCTGCCAC	ACT
GGGGAAAGGGAAGTCTG	CGT
TAGATGGGCTCTTCTTG	ACT.
TATGGAGCCCAAGGATGACC	ACT
	TGTGAACTGAAAAGTCAAG CTTGAACCTATTTCTGTTTT CTCCCAAGTTAGATTGGTTA CTTGATGTGGCTGAAGT GTGCTGTTGAAATCCTGGG AACCCTTTGTCAGCTGAA CAGGCTTTTGGCTAAGATCAAG AGTGAAGAATTTTCCCTATTAGAT AAGTCTAGCCAAGAACATTT CTCCACTCCTCTCATCAG GTTGCTGCCCGCTTTCC CTCTGTCACCCATGCTGGA ACCTCCTGGGCTCAAGC GGAAGGAATACTAAAGAACAA AGTAAGTGCTGTGATGCACC TAGCTGAGCATGGTGGC AGCATGGTGACAGC GGAAGGATACTAAAGAACAA AGTAAGTGCTGTGATGCACC TAGCTGAGCATGGTGGC ACCTCCTGGCCTCCCCT TCACAGAGCTGCCAGGG CAAAATTCTCCTGCCAC GGGGAAAGGGAAGTCTG TAGATGGGCTCTTCTTG

Please delete paragraph [0283] and replace it with the following paragraph:

[0283] The methods used to verify and allelotype the proximal SNPs of Table 29 are the same methods described in Examples 1 and 2 herein. The PCR primers and extend primers used in these assays are provided in Table 30 and Table 31, respectively. The methods used to verify and allelotype the proximal SNPs of Table 29 are the same methods described in Examples 1 and 2 herein. The PCR primers and extend primers used in these assays are provided in Table 30 and Table 31, respectively.

TABLE 30

dbSNP rs#	Forward PCR primer (SEQ ID NOS 733-778)	Reverse PCR primer <u>(SEQ ID NOS 779-824)</u>
726215	ACGTTGGATGAACTGAGCCCCATGAAATGC	ACGTTGGATGAAAACAGCAATTGAGAACAC
966783	ACGTTGGATGCTCCTGAATTTTAGCCATAC	ACGTTGGATGTACGCAATAGTTCCTGGGAG
998329	ACGTTGGATGGAAGAGCACATTATTTGCTGG	ACGTTGGATGACACACTGGTGTTTTGTCAG
1387472	ACGTTGGATGGAAGGCCTTGAATTGGAAC	ACGTTGGATGGTTCTGCTAGTGTCATCTTC
1484119	ACGTTGGATGGCAGCTACAATCATAAAGGG	ACGTTGGATGTGTGCCCTTAATAATGGTTG
1484120	ACGTTGGATGATGGTCATGGCATCCAGTTC	ACGTTGGATGGGCTGGTTTCTGACACTATC
1489479	ACGTTGGATGGGAGCATCAGTCATTTTGGG	ACGTTGGATGCACCAGGACATAACATGACG
1489480	ACGTTGGATGGGGTTGTGGAGAATCATTAC	ACGTTGGATGGGTGGCAGTAATCTTCACTT
1489481	ACGTTGGATGTCTCTGCAGTTGAGGAGATG	ACGTTGGATGTTGGGAAAGGCCATCAAGTC
1489482	ACGTTGGATGCTCTGGATAAAAGACTCAGC	ACGTTGGATGCCCTTCCAACAGCTATCTGG
1489483	ACGTTGGATGTTGGTTTGCTATCAATGAAG	ACGTTGGATGGATAGGTGTACACATATAGC
1489486	ACGTTGGATGAAAAAACACACCACAGCCCC	ACGTTGGATGCTTCGTATTTGGCTCTGACC
1552280	ACGTTGGATGATGAAAAGTGACACCCATCC	ACGTTGGATGTCTGAAGCTGTTGAATCAGG
1565288	ACGTTGGATGTAGCCAATTGGTGAACACTC	ACGTTGGATGCTGCCAGTCATAAGGCAAAG
1844334	ACGTTGGATGGCCAAGGAAACTAATTCCTG	ACGTTGGATGCACTTTGGAAGACAGTTCGG
1872203	ACGTTGGATGGTTGCATTAGCTGTTATTCTC	ACGTTGGATGCCAGCAATTCTATTTCAGAG
1905520	ACGTTGGATGCATGGTTTATACTTACTTACG	ACGTTGGATGGTTTATTCCTGTTTCCACAC
2029395	ACGTTGGATGGGAGGGAGACAAAGATTCAC	ACGTTGGATGGCAACAGTTTCACCTTTGGC
2029397	ACGTTGGATGCTCACAGTCCTGAAGACTTG	ACGTTGGATGTGGAAGTGAAGGAGAGAGC
2046777	ACGTTGGATGGGACTTCAAATATGGTTCAC	ACGTTGGATGTTAAGCCTGGGACTTTTGGG
2046778	ACGTTGGATGGTTCCCTTCCCCCATAAAAC	ACGTTGGATGCATGAAGCCTTATGCTTGAG
2054708	ACGTTGGATGCTAGGCATATCATGCCTCTG	ACGTTGGATGTTGAGCTCACTGTTACCTGC
2078403	ACGTTGGATGTGCTCAGGATCGACAGAC	ACGTTGGATGACTCGAGACAACCTACAAGG
2086832	ACGTTGGATGCTTTTGAGCATCACATTCCTC	ACGTTGGATGTGCCTAAGCACTGTATAACC
2129108	ACGTTGGATGAACTCCCAGTAAGTCCTTCC	ACGTTGGATGACTCAGGCAGTAACTCCAAC
2129111	ACGTTGGATGTACACTTTTCCCGCAAGACC	ACGTTGGATGGTCATGGACATCTACAGTATC
2170850	ACGTTGGATGGAAGGCCAATGCAAGGATAC	ACGTTGGATGAAGAACACACAAAAAAAAT
2279472	ACGTTGGATGGAGAAGAGCATTGGTTGCTG	ACGTTGGATGTGCCCACAAGTGCTATCTAC
2291304	ACGTTGGATGGTCTCAGGAAGGTTTAGAGG	ACGTTGGATGAAAAGACAAACGATATGGCC
2291305	ACGTTGGATGCATGATTTCAAAATCATGTTC	ACGTTGGATGGAGATGTACAGTATGAGTCC
2291306	ACGTTGGATGCAGCGACTAGTCATTAACCG	ACGTTGGATGCAGTTGGTTTCAACTCTGCC
2291309	ACGTTGGATGCATTGTTCCTACCATTC	ACGTTGGATGAAAGTGGTAAAGGAGAGGCG
2291310	ACGTTGGATGGTGCTTGATACTTGGCCTAC	ACGTTGGATGCAACTGGAAATTGCCGAAGC
2291311	ACGTTGGATGTCAACATTTACTCCTAGCTC	ACGTTGGATGATTTTGGGCTGTGGTCTTCC
2291312	ACGTTGGATGTGTATTCTCCTGCATCGCTC	ACGTTGGATGTCCAAGTTCAAGAACGACAC
2291313	ACGTTGGATGTTCGAGTTTACCGTATGGTG	ACGTTGGATGGATCACAGACAGGTCAGTTG
2306636	ACGTTGGATGCTGAGACCAGTCTGTGTTTG	ACGTTGGATGGTTTCCCATGACACTGTTCC
2306637	ACGTTGGATGCTACTACTATTTCTGGAGTC	ACGTTGGATGCTTATGCATTTCAACTGCCAC
	ACGTTGGATGGTAGATGCTTGAATCAATAAAG	ACGTTGGATGATAGCAGCTCCAGAACTAGG
2366912	ACGTTGGATGGAACTGTTGTTGAATGGGAC	ACGTTGGATGCAATACTTGTAAAATAGCAGC
2366913	ACGTTGGATGCTATCTGTATTCTCATGGCTG	ACGTTGGATGTTACCTAGTTCTGGAGCTGC
3769858	ACGTTGGATGCTACATGTCCATGGTTTGATG	ACGTTGGATGGCATCAACCTTTATGCCAAG
3769860	ACGTTGGATGGTATACAGAATATTGCATGCC	ACGTTGGATGGAACATCATTGAAGGTAAAG
3769863	ACGTTGGATGCAAGGATTTATTACATGCTG	ACGTTGGATGGTCATCAGGAGAAAGTAAGC
3816782	ACGTTGGATGGAGGAAACCAGAGCTTCAAG	ACGTTGGATGCAGCACGCTGTTTCTCAATG

3816849 ACGTTGGATGAACCAGCTCACCTCAGGAAC ACGTTGGATGTTTGTGGTGCCCATTCAAAC

TABLE 31

dbSNP rs#	Extend Primer (SEQ ID NOS 825-870)	Term Mix
726215	TTGAGAACACAGGATGC	ACT
966783	CTCCCATTTTGGTCTTG	ACG
998329	GGTGTTTTGTCAGTACAATT	ACG
1387472	ACTACAAACTCTTCCTTACC	CGT
1484119	GTTGTTTATGTTATGTTATGTGTT	ACT
1484120	TGTGCCTCAGTTTCTCC	CGT
1489479	GACAGCTGTAATTGTAGACC	ACT
1489480	CTCAATCACATTTACCCTC	ACT
1489481	TCTGATTGTTCCATTAATATCTG	ACT
1489482	CAGCTATCTGGAAATCTTGTTTGA	CGT
1489483	GTGTACACATATAGCAACCTCA	ACT
1489486	CTCTGACCTGTGAGCTAC	ACT
1552280	GCTGTTGAATCAGGATTTGATT	ACG
1565288	GGCAAAGAAACACTAGAAA	ACG
1844334	CAGTTCGGCAGTTTCTT	ACT
1872203	AAAAATCATGAAAAGGAGCATG	CGT
1905520	ACAAGTCTTTTCATGGTC	ACG
2029395	CAAAATGAAGGAACACTTATCA	ACG
2029397	AGCTCTGTTGGCACTTT	ACT
2046777	GAGCCTGATTATTTGTTTGGGTA	ACG
2046778	CTGTCATGATTGACAGGTCC	ACT
2054708	CCTGGGCCTGGAAGGCAAC	ACG
2078403	GGCTGGAGCAAGAATTA	ACG
2086832	CAATGTAATCCTTGGATAGAT	CGT
2129108	CAACTACATAGTCAGACTTT	ACT
2129111	TATACGCAATAGTTCCTGGG	ACT
2170850	GAACACACAAAAAAATTTAATCA	ACT
2279472	CTCTTTAAACCTGCATTTTC	ACT
2291304	CGATATGGCCATTTTGG	ACT
2291305	CATATTCACACAATGGGAAAA	CGT
2291306	CTGCCAACTATCAGCTT	ACT
2291309	GCGAGACCATGGCATATAACA	ACT
2291310	AACTTACACGTTTGTTGCTA	ACT
2291311	GTGGTCTTCCGGATATCA	ACG
2291312	CGACACAAATATGTAGTGGA	ACT
2291313	TGTCTTGCTACATTCCAGT	ACT
2306636	TCCAGTAAAATGGTTCCATAAGA	ACT
2306637	TCAACTGCCACAAAATG	ACT
2366911	TTCCTTTGTCCCATTCA	ACT
2366912	TGTAAAATAGCAGCTCCAGAA	CGT

2366913	ATTCTAAATGGAAAAAGAGCCA	ACG
3769858	TGCCCTGAATGTGCCTC	ACT
3769860	GGATAAGCATATGTAACTTTACG	CGT
3769863	AAGTAAAAAGGACATAAAAACCT	ACT
3816782	GTTGATGGAACAACATAAAA	CGT
3816849	GCCCATTCAAACATAAAG	ACT